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PRIOR PLILING DATE: 1004-03-10
PRIOR PLILING DATE: 2001-09-24
PRIOR PLILING DATE: 2001-09-24
PRIOR PLILING DATE: 2000-01-21
PRIOR PLILING DATE: 2000-01-21
PRIOR PLILING DATE: 2000-01-21
PRIOR PLILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR PLILING DATE: 2000-01-25
PRIOR PLILING DATE: 2000-02-03
PRIOR PLILING DATE: 2000-02-03
PRIOR PLILING DATE: 2000-04-27
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-26
PRIOR PLING DATE: 2000-03-26
PRIOR PLING DATE: 2000-03-28
                  Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3476
SOFTWARE: pt FL_genes Version 6.0
SEQ ID NO 1582
LENGTH: 154
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 1004-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-489-448-1704
; Sequence 1704, Application US/10489448
; GENERAL INFORMATION:
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Haley-Vicente, Dana
         PRIOR FILING DATE: 2000-02-28
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Ghosh, Malabika
Wang, Dunrui
Ma, Yunging
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70.00%
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Wang, Jian-Rui
Wehrman, Tom
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Xue, Aidong J
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Asundi, V...
Wang, Zhiwei
''ng, Gezhi
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; ORGANISM: Homo sapiens
US-10-489-448-1582
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Zhang, Jie
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: misc feature
LOCATION: (1)...(98)
LOCATION: (1)...(98)
COTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for US-10-489-448-3215
                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 3476
SOFTWARE: pt FL_genes Version 6.0
SEQ ID NO 3215
LENGTH: 98
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT PELLING DATE: 1004-03-10
PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR PELLING DATE: 2000-01-21
PRIOR PELLING DATE: 2000-01-22
PRIOR FILING DATE: 2000-01-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-11-25
PRIOR PELLING DATE: 2000-11-25
PRIOR PELLING DATE: 2000-11-25
PRIOR PELLING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/56,914
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APPLICANT: Haley-Vicente, Dana
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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PPLICATION NUMBER: PCT/USO1/03800
FILING DATE: 2001-05-05
APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1582, Application US/10489448 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weng, Gezhi
Haley-Vicente, Dana
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Zhou, Ping
Ghosh, Malabika
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Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Zhao, Qing A.
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ndi, Vinod
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Asundi,
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US-10-489-448-1582
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Matches:
Conservative:
Mismatches:
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                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/598,899
PRIOR FILING DATE: 2004-08-04
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 106
LENGTH
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PRIOR PILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 10/241,220
PRIOR APPLICATION NUMBER: US 10/177,488
PRIOR PILING DATE: 2002-06-19
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PSOOLHIPIB
CURRENT APPLICATION NUMBER: US/10/938,061
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 10/872,991
PRIOR APPLICATION NUMBER: US 10/872,991
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 106, Application US/10938061
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koeppen, Hartmut
Phillips, Heidi S.
Polakis, Paul
Spencer, Susan D.
Smith, Victoria
Williams, P. Mickey
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Hillan, Kenneth J.
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Sakanaka, Chie
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CORGANISM: Homo sapiens
US-10-938-061-106
                     TYPE: PRT

) ORGANISM: Homo sapiens

US-10-489-448-1704
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Best Local Similarity:
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Pred. No.:
                                                                                                      Alignment Scores:
     LENGTH: 103
                                                                                                                                                                                            Query Match:
DB:
                                                                                                                         Pred. No.:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
TITLE OF INVENTION: Treatment of Tumor
FILE REPERENCE: PSOOIRIPI
CURRENT APPLICATION NUMBER: US/10/936,626
CURRENT FILING DATE: 2004-09-08
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620 TyrCysCysArgValCysCysArgAlaCysCysLeuLeuCys 633
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Matches:
Conservative:
Mismatches:
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                                                                             US-10-775-481A-4 (1-57) x US-10-938-061-106 (1-690)
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: US 10/872,991

PRIOR APPLICATION NUMBER: US 10/872,972

PRIOR APPLICATION NUMBER: US 10/241,220

PRIOR FILING DATE: 2002-05-11

PRIOR PILING DATE: 2002-05-11

PRIOR PILING DATE: 2002-06-19

PRIOR PILING DATE: 2002-06-19

PRIOR PILING DATE: 2002-06-19

PRIOR PILING DATE: 2001-06-20

PRIOR PILING DATE: 2001-06-20

PRIOR PILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-20

PRIOR PILING DATE: 2001-06-20

PRIOR PILING DATE: 2001-09-18

PRIOR PILING DATE: 2001-09-18

PRIOR PILING DATE: 2004-09-18

PRIOR PILING DATE: 2004-09-16

PRIOR PILING DATE: 2004-09-04

**SEQ ID NO 106

**LENGTH: 690
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                                                                                                                                                                                                                                                                            Sequence 106, Application US/10936626
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, P. Mickey
Wu, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Koeppen, Hartmut
Phillips, Heidi S.
Polakis, Paul
Spencer, Susan D.
Smith, Victoria
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Query Match:
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Pred. No.:
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APPLICANT: EXELIZIS, INC.
TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE FILE REFERENCE: EXO5-004C-PC
CURRENT APPLICATION NUMBER: PCT/USO5/03560
CURRENT FILING DATE: 2005-01-27
PRIOR PILING DATE: 2004-01-28
PRIOR FILING DATE: 2004-01-28
SEQ ID NO 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 3398
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 38-21 (53629) A
CURRENT APPLICATION NUMBER: US/60/643,717
CURRENT FILING DATE: 2005-01-12
NUMBER OF SEQ ID NOS: 19247
SEQ ID NO 5307
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Matches:
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Indels:
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Matches:
      CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 285
LENGTH: 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US05-03560-6; Sequence 6, Application PC/TUS0503560; GENERAL INFORMATION:
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; ORGANISM: Kluyveromyces lactis
US-60-643-717-5307
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53.85
53.85
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US-10-287-436A-285
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                             TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Olsen, Byron
TITLE OF INVENTION: Treatment of Obesity and Diabetes
TITLE OF INVENTION: Treatment of Obesity and Diabetes
TILE REFERENCE: GTC-223
CURRENT APPLICATION NUMBER: US/11/060,291
CURRENT PILING DATE: 2005-02-17
PRIOR FILING DATE: 2004-02-19
PRIOR FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE PATENTIN VERSION 3.3
SEQ ID NO 6
LENGTH: 1071
APPLICANT: Olsen, Byron

TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the TITLE OF INVENTION: Treatment of Obesity and Diabetes
FILE OF INVENTION: Treatment of Obesity and Diabetes
FILE REFERENCE: GTC-223 PCT
CURRENT APPLICATION NUMBER: PCT/USOS/05406
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/545,790
PRIOR FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.3
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Sequence 285, Application US/10287436A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEMMATION ARTHRITIS
TITLE OF INVENTION: RHEMMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||
261 CysCysGlyAlaCysThrCysThrCysGlydlyCys 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TGCTGTGAATTGTGTTGTAATCCTGCTTGTAACGGGTGC 54
                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TGCTGTGAATTGTGTTGTAATCCTGCTTGTAACGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-775-481A-4 (1-57) x PCT-USO5-05406-6 (1-1071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-775-481A-4 (1-57) x US-11-060-291-6 (1-1071)
                                                                                                                                                                                                                                                                                                                                       2.22
54.00
53.85%
53.85%
42.86%
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54.00
53.85%
53.85%
42.86%
                                                                                                                                                                                                                LENGTH: 1071
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Bapiens
US-11-060-291-6
                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                             PCT-US05-05406-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-060-291-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
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41 AsnileCysCysArgArgCysCysAsnCysCysCysSer 53
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52.00
61.54%
53.85%
                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (2)..(2)
                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_95597; Strand=-; Position=3-
US-60-655-875-169174
                                                                                                                                                                                                                                                      APPLICANT: Kovalic, David

APPLICANT: Lu, Maolong

APPLICANT: Macater, James

APPLICANT: Miller, Nancy

APPLICANT: Williams, Deryck

APPLICANT: Williams, Deryck

APPLICANT: Wundin, Mark

APPLICANT: Vaudin, Mark

APPLICANT: Vaudin, Mark

APPLICANT: Wundin, Mark

APPLICANT: Wundin, Mark

APPLICANT: Wun Wei

TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF

FILE REFERENCE: 38-21 (53885)

CURRENT APPLICATION UNMER: US/60/655,875

CURRENT FILING DATE: 2005-02-24

NUMBER OF SEQ ID NOS: 171306

SEQ ID NO 169174

LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
                                                                                                                                                                                            ||||||||||
77 TyrLysGlnSerLysLysLeulleHisSerSerAsnLeuTyrTyr 91
                                                                                                                                                                    46 TACAAGCAGGATTACAACACAAATTCACAGCAGTAATTGCTACTAT
                     423
10
0
0
0
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AsnIleCysCysArgArgCysCysAsnCysCysCysSer 23
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                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                    US-10-775-481A-4 (1-57) x US-60-643-717-5307 (1-423)
                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-60-655-875-163386
; Sequence 163386, Application US/60655875
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Heterodera glycines
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boukharov, Andrey
APPLICANT: Boukharov, Andrey
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maclong
APPLICANT: Miler, Nancy
APPLICANT: Millams, Deryck
APPLICANT: Williams, Deryck
APPLICANT: Williams, Deryck
APPLICANT: Wulliams, Deryck
APPLICANT: Wulliams, Wei
                  3.16
53.00
66.67%
66.67%
50.96%
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52.00
61.54%
53.85%
41.27%
                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                       RESULT 14
US-60-655-875-169174
Alignment Scores:
Pred. No.:
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; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_89809; Strand=-; Position=0-4 US-60-655-875-163386
                                                                                                                                                                                                                                                                                         LOCATION: (2)...(2)

LOCATION: (1)...(2)

FEATURE:
NAME/KEY: misc feature
LOCATION: (4)...(4)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (14).

UNTER INFORMATION: Xaa can be any naturally occurring amino acid FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)...(21)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 163386
LENGTH: 158
                                                                                                                                                                    TYPE: PRT
ORGANISM: Heterodera glycines
```

10 AATTACTGCTGTGAATTGTGTTGTAATCCTGCTTGTAAC 48 US-10-775-481A-4 (1-57) x US-60-655-875-163386 (1-158) Length: Matches: Conservative: Mismatches: Indels:

Search completed: March 26, 2005, 18:03:12 Job time : 30 secs

Appl

Sequence 5, 1 Sequence 5, 1 Sequence 5, 1

Length

Query Match

Sequence 5, Sequen

Sequence 5, Sequence 23, Sequence 20,

100.00 100.00 100.00 95.22 95.23

Sequence 31,

Sequence

Sequence

Sequence Sequence

Sequence 31, Sequence 20,

Run on:

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Result
No.
                                                                                                                                                                                                              March 26, 2005, 16:39:19; Search time 78.4963 Seconds (without alignments) 282.715 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/USOG_COMB.pep:*

10: /
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6959266 seqs, 1168006243 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                           NSSNYCCELCCNPACNGCY 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                      US-10-775-481A-5
                                      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                 OM protein
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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Appli Appli Appli Appli Appli Appli

Sequence

Sequence Sequence Sequence

Sequence

PCT-USO4-03765-5
PCT-USO4-12232-5
US-08-648-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-263-4778-5
US-09-21-521-23
US-08-39-114-23
US-10-766-735-16
US-10-766-735-96
US-10-766-735-96
US-10-766-735-96
US-10-766-735-97
US-10-766-735-97
US-10-766-735-97
US-10-766-735-87

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

ALIGNMENTS

Sequence

Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Park, Jason
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
APPLICANT: Schulz, Stephanie
APPLICANT: Schulz, Stephanie
APPLICANT: Lubbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-168 PC1
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/446,730
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5

```
ATTORNEY AGENT INFORMATION:
NAME: Deluca, Mark:
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMUNICATION INFORMATION:
TELECHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,477
                                          RESULT 3
US-08-468-449B-5
; Sequence 5, Application US/08468449B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Novel Sequence US-08-468-449B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09263477 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-263-477-5
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                                                                                                                                                                                                                                   ch 100.0%; Score 126; DB 1; Length 19; l Similarity 100.0%; Pred. No. 1.7e-06; 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5. Application PC/TUS9412232
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 126; DB 1;
100.0%; Pred. No. 1.7e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Philadelphia STATE; Pennsylvania COUTTY: Philadelphia COUNTY: USA ZIP: 19103
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION NUMBER: PCT/US94/12232 FLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Defluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-136
TELECOMMUNICATION INFORMATION:
TELEPAX: 215-568-3100
TELEPAX: 2
                                                                                                                                                                                                                                                                                                                                                                                                            1 NSSNYCCELCCNPACNGCY 19
                                                                                                                                                                                                                                                                                                                                                                     1 NSSNYCCELCCNPACNGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; So
Best Local Similarity 100.0%; P:
Matches 19; Conservative 0;
                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 19 amino acids
amino acid
GY: linear
                                                                                                                                 ; OTHER INFORMATION: ST ID PCT-US04-03765-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein PCT-US94-12232-5
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Best Local Similarity
Matches 19; Conserv
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LENGTH: 19
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APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
FILE REPERENCE: TUTU-188 TO 1995-06-06
CURRENT APPLICATION NUMBER: US/08/468,449B
PRIOR APPLICATION NUMBER: 08/141,892
PRIOR PADPLICATION NUMBER: 08/141,892
PRIOR FILING DATE: 1993-10-26
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 5
LENGTH: 19
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TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STRTE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
COMPUTER: PEN PC compatible
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Gaps

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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
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                                                                                                                                                                                         Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
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Pred. No. 1.7e-06;
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illarity 100.0%; Pred. No. 1.7e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/583,447A FILING DATE: 05-JAN.1996
APPLICATION NUMBER: US 08/141,892 FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684 FILING DATE: 17.7ul-2003 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     US-10-621-684-5; Sequence 5, Application US/10621684; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          1 NSSNYCCELCCNPACNGCY 19
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                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
  PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 54
SOTWARE: Patentin version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
STATE: Pennsylvania
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                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-724-983-5
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Matches 19; Conserv
                                                                                   LENGTH: 19
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GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION:
FILE REFERENCE: TJU-2444
CHORRENT APPLICATION NUMBER: US/09/724,983
CHORRENT PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 08/468,449
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CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & Norris STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
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  Length 19;
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                                                                                                                                                                                                        3-09-263-47/A-5
Sequence 5, Application US/09263477A
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
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Query Match 100.0%; Score 126; DB 16; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 19; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Wordferfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,477A
FILING DATE: 05-Mar-1999
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-Mar-1996
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ'ID NO: 5:
US-09-263-477A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                        1 NSSNYCCELCCNPACNGCY 19
                                                                                 1 NSSNYCCELCCNPACNGCY 19
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acidd
TYPE: amino acid
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COUNTRY: USA
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Best Local Similarity 100.
Matches 19; Conservative
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US-09-263-477A-5
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APPLICANT: Lebens, Michael
TITLE OF INVENTION: IMMUNGENS FOR STIMULATING MUCOSAL
TITLE OF INVENTION: IMMUNITY
NUMBER OF SEQUENCES: 5.1
ADDRESSEE: Knobbe, Martens, Olson and Bear
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CUMURINI USAN

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/085,126
FILING DATE: 25-UNN-1993
CLASSIPFCATION: 435
ATTORNEY AGGNT INFERMATION:
NAME: COOPER, IYPE P.
RECISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LADNER=10
TELEPHONE: 202-628-5197
TELEFRAN: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120; DB 4;
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.2%; Scc. 94.7%; Pred. No. ...
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APPLICATION NUMBER: US/08/342,241A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                             STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-342-241A-31
; Sequence 31, Application US/08342241A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSSNYCCELCCNPACTGCY 19
  APPLICANT: LADNER, Robert C. APPLICANT: CANNON, LATICK B. TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 236 CORRESPONDENCE ADDRESS: ADDRESSE: BROWDY AND NEIMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.2
Best Local Similarity 94.7
Matches 18; Conservative
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PCT-USO2-09551-23
Sequence 23, Application PC/TUS0209551
Sequence 23, Application PC/TUS0209551
GENERAL INFORMATION:
APPLICANT: SYNERGY PHARMACEUTICALS
TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS
FILE REFERENCE: 81361/141030
CURRENT PELLION UMBER: PCT/US02/09551
CURRENT PELLION DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 23
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 126; DB 33; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: heat stable toxin peptide Ib
US-10-775-481A-5
                                     APPLICANT: Waldman, Scott A.
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Schulz, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Lubbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-0168 USI
CURRENT APPLICATION NUMBER: US/10/775,481A
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                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 19
                                                                                                                                                                                                                                       CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/446,730
PRIOR FILING DATE: 2003-02-10
; Sequence 5, Application US/10775481A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-085-126-20
; Sequence 20, Application US/08085126
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
PCT-US02-09551-23
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| Sequence 31, Application US/09291520
| GENERAL INFORMATION:
| APPLICANT: Hologrem, Jan
| APPLICANT: Lebens, Michael
| TITLE OF INVENTION: IMMUNITY |
| TITLE OF INVENTION: IMMUNITY |
| NUMBER OF SEQUENCES: 51 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Knobbe, Martens, Olson and Bear ADDRESSEE: Knobbe, Martens olson and Bear STREET: 620 Memport Center Drive 16th Floor CITY: Newport Beach |
| STATE: GA |
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ATTORNEY/AGENT INFORMATION:
NAME: MCCCMmack, Myra H
REGISTRATION NUMBER: 36,602
TELECOMMUNICATION INFORMATION:
TELEPHOND: 619-235-850
TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFFICATION
PRIOR APPLICATION
APPLICATION NUMBER: 08/342,241
                                                                                                                                                                                                                                                                                                                           1 NSSNYCCELCCNPACNGCY 19
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
      LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                            single
                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                 TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                            ; MULECULE 111
US-08-438-114-20
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APPLICANT: CANNON, Larick E.
TITLE OF INVENTION: CHELYDRYZYMES AND NEPAZYMES, AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 240
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,114
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/308,793
APPLICATION NUMBER: US 08/308,793
FILING DATE: 19-SEP-1994
PRIOR APPLICATION NUMBER: US 08/085,126
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 7;
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                              NAME: MCCOTMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: HOLMG.001A
TELECOMMUNICATION:
TELEPHONE: 619-235-850
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LADNER=10B
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REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                             31:
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                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.7
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
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                                                               APPLICANT: LOBERS, MICHAEL
TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
TITLE OF INVENTION: IMMUNITY
FILE REFERENCE: HOLMG.001DV1
CURRENT APPLICATION NUMBER: US/09/291,520A
CURRENT FILING DATE: 1999-04-04
FEALLER APPLICATION NUMBER: 08/342,241
EARLIER FILING DATE: 1994-11-17
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09525715
; Sequence 2, Application US/09525715
; GENERAL INFORMATION:
; APPLICANT: Johnson, David
; APPLICANT: Losco, Particia
; APPLICANT: Hagen, Else Kruger
; APPLICANT: Hagen, Else Kruger
; APPLICANT: Hagen, Else Kruger
; APPLICANT: Desal, Vinay
; TITLE OF INVENTION: Transplantable Sarcoma
; FILE REFERENCE: Transplantable Sarcoma
; FILE REFERENCE: Transplantable Sarcoma
; FILE REFERENCE: Transplantable Sarcoma
; FILE REFILING DATE: 1999-03-14
; PRIOR FILING DATE: 1999-03-15
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIN Ver. 2.1
; SRQ ID NO 2.
Sequence 31, Application US/09291520A
GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NSSNYCCELCCNPACTGCY 19
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, ORGANISM: Escherichia coli
US-09-525-715-2
                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: E. coli
US-09-291-520-31
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0; Gaps 1, Indels 0; Mismatches Score 120; Pred. No. 7 1 NSSNYCCELCCNPACNGCY 19 1 NSSNYCCELCCNPACTGCY 19 Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative C

Search completed: March 26, 2005, 17:10:17 Job time: 79.4963 secs

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Sequence 1249, Application US/11066697
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Brin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
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US-11-066-697-1249
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3215, Ap
1582, Ap
106, App
106, App
6, Appl
6, Appl
6, Appl
6, Appl
6, Appl
106, Appl
106, Appl
106, Appl
106, Appl
106, Appl
107, Appl
108, Appl
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581, App
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56787, A
135230,
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1247, Ap
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                                                                                                                    March 26, 2005, 16:44:35; Search time 5.89416 Seconds (without alignments) 187.395 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132098,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
Sequence 6
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Sequence
Sequence
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Sequence
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1: /cgn2 6/prodats/1/paa/PCT NEW COMB.pep:*

2: /cgn2 6/prodats/1/paa/US06 NEW COMB.pep:*

3: /cgn2 6/prodats/1/paa/US08 NEW COMB.pep:*

4: /cgn2 6/prodats/1/paa/US08 NEW COMB.pep:*

5: /cgn2 6/prodats/1/paa/US08 NEW COMB.pep:*

6: /cgn2 6/prodats/1/paa/US10 NEW COMB.pep:*

7: /cgn2 6/prodats/1/paa/US11 NEW COMB.pep:*

8: /cgn2 6/prodats/1/paa/US11 NEW COMB.pep:*
           version 5.1.6
- 2005 Compugen Ltd.
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US-11-066-697-1249
US-60-655-875-128831
US-10-489-448-1518
US-10-489-448-1518
US-10-489-448-1704
US-10-936-626-106
US-10-936-626-106
US-11-060-291-6
US-11-060-291-6
US-10-287-169174
US-60-655-875-169174
US-60-655-875-163386
US-10-184-644-581
US-10-192-007-581
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             260697 segs, 58133403 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           US-10-775-481A-5
126
1 NSSNYCCELCCNPACNGCY 19
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
             GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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Match Length
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                                                                                    OM protein
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Maximum DB
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                                                                                                                        Run on:
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Sequence 1646, Ap
Sequence 1646, Ap
Sequence 59727, A
Sequence 3, Appl
Sequence 12, Appl
Sequence 165998,
Sequence 139718,
Sequence 139718,
Sequence 153943,
Sequence 24057, A
Sequence 269, Appl
Sequence 16972,
Sequence 169804,
Sequence 162472,
Sequence 169804,
Sequence 168914,
Sequence 168914,
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 220, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCREMENTATION:
GENERAL INCREMENTATION:
APPLICANT: Balloul, Jean Marc
APPLICANT: Balloul, Stephane
APPLICANT: Geist, Michel
APPLICANT: Silvestre, Nathalle
APPLICANT: Silvestre, Nathalle
APPLICANT: Erbs, Philippe
TITLE OF INVENTION: Poxylius With Targeted Infection Specificity
TITLE OF INVENTION: Poxylius With Targeted Infection Specificity
FILE REFERENCE: 032751-15
CURRENT FILING DATE: 2004-09-07
FRIOR PELICATION NUMBER: US 09/832,899
FRIOR PELICATION NUMBER: US 09/832,899
FRIOR PELICATION NUMBER: DO 040109.7
FRIOR APPLICATION NUMBER: EP 0040109.7
FRIOR APPLICATION NUMBER: EP 01440009.7
FRIOR PILING DATE: 2000-04-14
FRIOR PELING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 52
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LIBROTH: 18-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.8%; Score 98; DB 6; Length 18; Best Local Similarity 93.3%; Pred. No. 1.7e-06; Matches 14; Conservative 0; Mismatches 1; Indels
US-10-450-763-42525
US-10-450-763-1646
US-10-68-476-3
US-10-934-728-22
US-60-655-875-137235
US-60-655-875-137235
US-60-655-875-137235
US-60-655-875-133718
US-60-655-875-133718
US-10-450-763-38696
US-10-450-763-38696
US-10-450-763-4957
US-10-287-4364-269
US-10-287-1392
US-60-655-875-169804
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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; Sequence 24, Application US/10934728
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Sta ligand US-10-934-728-24
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Gaps

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LOCATION: (1)...(98)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
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CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 1004-03-10
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR PLICATION NUMBER: US 09/488,725
PRIOR PLICATION NUMBER: US 09/488,725
PRIOR PLING DATE: 2000-01-22
PRIOR PLING DATE: 2000-01-2-22
PRIOR PLING DATE: 2000-01-2-22
PRIOR PLING DATE: 2000-01-22
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2000-01-21
PRIOR PLING DATE: 2000-01-20
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Mucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-489-448-1582
; Sequence 1582, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
                                                                                                         Sequence 3215, Application US/10489448 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haley-Vicente, Dana
                                                                                                                                                                                    Tang, Y. Tom
Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Zhao, Qing A.
Wang, Jan-Rui
Wehrman, Tom
Zhou, Ping
Ghosh, Malabika
Wang, Dunrui
Ma, Yunqing
Asundi, Yinod
Wang, Zhiwei
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-489-448-3215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_55254; Strand=-; Position=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guo, Liang
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maolong
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Williams, Deryck
APPLICANT: Williams, Deryck
APPLICANT: Wudin, Mark
APPLICANT: Vaudin, Mark
APPLICANT: Wudin, Mark
APPLICANT: Wudin, Mark
APPLICANT: Wudin, Mark
APPLICANT: Wudin, Mark
APPLICANT: Wumin Mark
APPLICANT: Numin Mark
APPLICANT: 
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APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 500662002301
CURRENT FALING DATE: 2005-02-25
PRIOR FILING DATE: 2005-02-25
PRIOR FILING DATE: 2006-09-07
PRIOR PLING DATE: 1999-09-10
PRIOR PLING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE PARENTENTON NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
SOFTWARE PARENTENTON NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
SOFTWARE PARENTENTON NUMBER: 60/159,783
FRIOR FILING DATE: 1999-10-15
SOFTWARE PARENTENTON NUMBER: 10/159,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Peptide US-11-066-697-1249
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Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 SSNHCCTSSSCCNHSSNRC 257
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ORGANISM: Heterodera glycines
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR PLICATION NUMBER: US 09/488,725
PRIOR PLING DATE: 2000-01-21
PRIOR PLING DATE: 2000-01-21
PRIOR PLING DATE: 2000-01-22
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-22
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-04-27
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-03
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APPLICANT: Haley-Vicente, Dana
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: US/10/489,448
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CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 10/872,991
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Zhang, Zemin
Sakanaka, Chie
Chuntharapai, Anan
Reed Chae J.
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Hillan, Kenneth J.
Koeppen, Hartmut
Phillips, Heidi S.
Polakis, Paul
Spencer, Susan D.
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CCELCCNPACNGC 18
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ORGANISM: Homo sapiens
US-10-489-448-1704
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haley-Vicente, Dana APPLICANT: Dramac, Radoje T TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides CURRENT APPLICATION NOWBER: US/10/489,448
FILE REFERENCE: 810CTP PCT CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 2000-09-24
FRIOR FILING DATE: 2000-09-24
FRIOR PILING DATE: 2000-09-24
FRIOR PELING DATE: 2000-01-21
FRIOR PELING DATE: 2000-01-21
FRIOR APPLICATION NUMBER: US 09/55,317
FRIOR PELICATION NUMBER: PCT/US0/35017
FRIOR PELING DATE: 2000-01-25
FRIOR PELING DATE: 2000-01-25
FRIOR PELING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: PCT/US0/102623
FRIOR PELING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: US 09/491,404
FRIOR APPLICATION NUMBER: US 09/560,875
FRIOR APPLICATION NUMBER: US 09/560,875
FRIOR PELING DATE: 2000-04-27
FRIOR APPLICATION NUMBER: US 09/560,875
FRIOR PELING DATE: 2000-04-27
FRIOR PELING DATE: 2000-04-27
FRIOR PELING DATE: 2000-04-27
FRIOR PELING DATE: 2000-02-08
FRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1704, Application US/10489448
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
                                                                                                                Zhou, Ping
Ghosh, malabika
Wang, Dunrui
Ma, Yunqing
Asundi, Vinod
Wang, Chiwei
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Ghosh, Malabika
Wang, Dunrui
Ma, Yunging
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 CCQPCCRPAC 134
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US-10-489-448-1582
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Best Local Similarity
Matches 7; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-489-448-1704
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LENGTH: 1071
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                                 LENGTH: 690
   SEQ ID NO 106
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TITLE OF INVENTION: Treatment of Tumor
TITLE OF INVENTION: Treatment of Tumor
FILE OF INVENTION: Treatment of Tumor
FILE REPERBUCE: P5001RLP1
CURRENT APPLICATION NUMBER: US/10/936,626
CURRENT APPLICATION NUMBER: US/10/872,991
PRIOR APPLICATION NUMBER: US 10/872,991
PRIOR FILING DATE: 2004-06-21
PRIOR FILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/391,880
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2004-03-26
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Pred. No. 13;
1; Mismatches 6; Indels
PRIOR FILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US 10/872,972

PRIOR FILING DATE: 2004-06-21

PRIOR PILING DATE: 2002-06-11

PRIOR PILING DATE: 2002-09-11

PRIOR PILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US 10/177,488

PRIOR FILING DATE: 2002-06-19

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-39

PRIOR FILING DATE: 2004-03-16

PRIOR PILING DATE: 2004-03-6

PRIOR PILING DATE: 2004-03-6

PRIOR PILING DATE: 2004-03-6

NUMBER OF SEQ ID NOS: 154
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APPLICANT: Cairns, Belinda
APPLICANT: Crentz, Gretchen
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi S.
APPLICANT: Spencer, Susan D.
APPLICANT: Spencer, Susan D.
APPLICANT: Sinith, Victoria
APPLICANT: Mulliams, P. Mickey
APPLICANT: Wulliams, P. Mickey
APPLICANT: Wulliams, P. Mickey
APPLICANT: Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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US-10-938-061-106
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RESULT 10

US-11-060-291-6

J Sequence 6 Application US/11060291

GENERAL INFORMATION:

APPLICANT: Olsen, Byron

TITLE OF INVENTION: Treatment of Obesity and Diabetes

TITLE OF INVENTION: Treatment of Obesity and Diabetes

TITLE OF INVENTION: Treatment of Obesity and Diabetes

FILE REPERENCE: GTC-223

CURRENT PILING DATE: 2005-02-17

PRIOR PILING DATE: 2004-02-19

PRIOR PILING DATE: 2004-02-19

PRIOR PILING DATE: 2004-02-19

SOFTWARE: PatentIn version 3.3

SEQ ID NO 6

LENGTH: 1071

TYPE: PRT

CORDANISM: Homo sapiens

US-11-060-291-6
                                                                                                                                                                                                                                                                          Sequence 6, Application PC/TUS0505406

Sequence 6, Application PC/TUS0505406

GENERAL INFORMATION:
APPLICANT: Olsen, Byron
TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the TITLE OF INVENTION: Treatment of Obesity and Diabetes
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/545,790
PRIOR FILING DATE: 2004-02-19
NUMBER OF SEQ ID MOS: 23
SOFTWARE: Patentin version 3.3
SEQ ID NO 6
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Pred. No. 19;
0; Mismatches 6; Indels
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                                                                            Length 690
                                                                                                                    6; Indels
                                                                            DB 6;
13;
                                                                                                                    1; Mismatches
                                                                              Score 54;
Pred. No.
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53.8%;
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                                                                            Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
TYPE: PRT
CORGANISM: Homo sapiens
US-10-936-626-106
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ORGANISM: Homo sapiens
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APPLICANT: Du, Zijing
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Kovalic, David
APPLICANT: Maolong
APPLICANT: Miller, Nancy
APPLICANT: Willier, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Wadin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (2)...(2)
OTHER INFORMATION: Xaa can be
                                                                                                                   TYPE: PRT
ORGANISM: Heterodera glycines
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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      FILE REFERENCE: 38-21 (53885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Boukharov, Andrey
                                                                                                                                                                                                                                                                                                                4 NYCCELCCNPACN 16
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Best Local Similarity
Matches 7; Conserv
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EXELIZIS, INC.
TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE FILE REFERENCE: EXO5-004C-PC
CURRENT PAPLICATION NUMBER: PCT/USO5/03560
CURRENT FILING DATE: 2005-01-27
PRIOR APPLICATION NUMBER: US60/539,837
PRIOR FILING DATE: 2006-01-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                      APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: METHOD POR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REPERENCE: 10872.514696
CURRENT PELLING DAFE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: PASCESO FOR Windows Version 4.0
SEQ ID NO 285
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Pred. No. 54;
0; Mismatches
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                                    Sequence 285, Application US/10287436A GENERAL INFORMATION:
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8 Matches 7; Conservative
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Miller, Nancy
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Lu, Maolong
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Du, Zijing
Guo, Liang
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RESULT 11
US-10-287-436A-285
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APPLICANT:
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FEATURE:
; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_95597; Strand=-; Position=3-
US-60-655-875-169174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATE: Vaudin, Mark
APPLICATE: W. Wei
TITLE OF INVENTION: ML METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21 (53885)
CURRENT APPLICATION NUMBER: US/60/655,875
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 163386
TYPE-
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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                                                                                                                                                                                                                                                        5; Indels
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Pred. No. 6.1;
1; Mismatches
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llarity 53.8%; Pred. No. 6.3;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          naturally
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 169174
LENGTH: 152
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OTHER INFORMATION: Xaa can be any
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa can be any
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APPLICANT: Chen,Jahan
APPLICANT: Ghen,Jahan
APPLICANT: Goddard,Audrey
APPLICANT: Goddard,Audrey
APPLICANT: Goddard,Audrey
APPLICANT: Goddard,Audrey
APPLICANT: Goddard,Audrey
APPLICANT: Goddard, Pan,James
APPLICANT: San,James
APPLICANT: San,James
APPLICANT: Matamaba,Colin K.
APPLICANT: Zhang,Zemin
APPLICANTON NUMBER: 105/106,484
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/059266
PRIOR APPLICATION NUMBER: 60/059266
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063540
PRIOR APPLICATION NUMBER: 60/063540
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063541
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: PIRING D
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Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 6; Indels
RESULT 15
US-10-184-644-591
Sequence 581, Application US/10184644
GENERAL INFORMATION:
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                                                                                                                                                           APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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CORGANISM: Homo Sapien
US-10-184-644-581
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Search completed: March 26, 2005, 17:11:53 Job time : 6.89416 secs

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March 26, 2005, 16:39:19; Search time 437.927 Seconds (without alignments) 282.715 Million cell updates/sec
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548.
1 MSGSQLWAAVLLLUVLQSAQ......LRTIATDECELCINVACTGC 106
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1: /cgn2 6/ptodata/1/paa/PCTUS COMB.pep:*
2: /cgn2 6/ptodata/1/paa/US06 COMB.pep:*
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5: /cgn2 6/ptodata/1/paa/US081 COMB.pep:*
6: /cgn2 6/ptodata/1/paa/US081 COMB.pep:*
7: /cgn2 6/ptodata/1/paa/US082 COMB.pep:*
9: /cgn2 6/ptodata/1/paa/US083 COMB.pep:*
10: /cgn2 6/ptodata/1/paa/US083 COMB.pep:*
11: /cgn2 6/ptodata/1/paa/US087 COMB.pep:*
11: /cgn2 6/ptodata/1/paa/US082 COMB.pep:*
11: /cgn2 6/ptodata/1/paa/US092 COMB.pep:*
11: /cgn2 6/ptodata/1/paa/US092 COMB.pep:*
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/ptodata/1/paa/US099B_COMB.pep:*
/ptodata/1/paa/US100_COMB.pep:*
/ptodata/1/paa/US101_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6959266 seqs, 1168006243 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	,	Query	•		!	
. ON	Score	Match	Length	B :	ID	Description
н,	548	100.0	106		PCT-US04-03765-55	ce 55
0	548	100.0	106	C) [US-10-775-481A-55	sence 55
m <	358		111	- 1	US-60-248-592-71	nence 71
* u	9 20		122	•	DOT-11504-03766-66	sednence zz
n w	350		112		PCT-US04-36404-145	5.4
7	356		112		US-10-170-205E-19124	Sequence 19
80	356		112	0		'n
O	356		112	[7]	US-10-700-439-145	Sequence 145, App
10	356		112	C1		Sequence 56, Appl
11.	356		112		US-60-453-050-12227	Sequence 12227, A
77.	9 L		112	- 1	** **	Sequence 12227, A
5 F	356		112			Sequence 12227, A
151	306	5.00	112	• (•	Sequence 1020, Ap
16	306		6 6	, ,	US-60-197-873-26398	Sequence 26398. A
17	252.5		109			Sequence 6, Appli
18	166.5		115		PCT-US04-18751-70	Sequence 70, Appl
19	166.5	30.4	115	וח	US-09-834-366-17911	Sequence 17911, A
200	166.5	30.4	115	so v	US-09-981-353-61	Sequence 61, Appl
21	166.5	4.00	115	O L	•	Sequence 22, Appl
2.6	166.5	7.00	115	• u	_	Sequence 19125, A
24	166.5	30.4	115) Œ	US-10-262-473-12	Sequence 22, Appl
25	166.5	30.4	115	, 0	US-10-479-606-4	Sequence 4, Appli
. 56	166.5	30.4	115		US-60-197-873-17911	Sequence 17911, A
27	166.5	30.4	115			Sequence 61, Appl
28	166.5	30.4	115		US-60-453-050-12228	Sequence 12228, A
. 50	166.5		115			Sequence 12228, A
30	166.0		CTT	· .	••	Sequence 12228, A
3.5	152.5		0 0	•	DCT-11504-1874-180	Segrence 190, App
3 6	120		102		PCT-US04-18751-71	Sequence 71. Appl
34	120		102	œ	US-10-262-473-14	
32	120	_	108		PCT-US04-18751-72	
36	120		108	œ.	US-10-262-473-16	a)
37	114	- 2	24		- 4	
20 00	ט ט		119	v	US-09-791-537-68439	
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4.4	. 7.0		9 6	◂	US-09-925-299-1162	110
42	90		15		PCT-US04-18751-48	48,
43	89	- :	17	_	US-60-160-203-3643	e 364
44	84	15.3	16	н,	PCT-US02-09551-20	dnenc
45	89		16		PCT-US04-18751-73	equence 73,
					ALIGNMENTS	
RESULT	1 - 02766-	u				
ະຄ	-UsV4-Us/65-55 equence 55, Applic	oo Applica	cation PC/TUS0403	/TUS	30403765	
GENER	AL INFOR	MATION:				
, APPL	ICANT: W	aldman,	. Waldman, Scott A.	 4		
APPL	ICANT:	Pitari,	Giovan	<u>.</u>	Mario	
APPL	CANT:	Schul?	Stenha	9		
APPL	CANT:	Wolfe,	Henry R			
, APPL	ICANT:	Lubbe,	Wilhelm			
TITE	TITLE OF INVENTION: 1	ENTION:	The Use	e Of	: GCC Ligands	
CURRENT	ENT APPL	ICATION	ZI-IOS	ļΩ	CT/US04/03765	
, CURRI	BNT FILI	NG DATE	2004	Ø	10	
, PRIOR AE	R APPLICATION NUMBER: US	ATION N	UMBER:		0/446,730	
; PRIO	R FILING	DATE:	E: 2003-02	-10		
SOFT	WARE: Fa	BLSEO E	or Windows	8MO	Version 4.0	
SEQ ID NO	NO 55	1	1	,		

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US-60-245-228-223
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TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000961
CURRENT APPLICATION NUMBER: US/60/248,592
CURRENT APPLICATION NUMBER: 105
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                         1 MSGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPD 60
                                                                                                                                                                                                                       1 MSGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPD 60
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                                                                                          Query Match 100.0%; Score 548; DB 1; Length 106; Best Local Similarity 100.0%; Pred. No. 2.9e-54; Matches 106; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                       61 VCYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/10775481A
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Wolfe, Henry R.
APPLICANT: Wolfe, Henry R.
APPLICANT: Wolfe, Henry R.
FILE REFERENCE: 08321-0168 US1
CURRENT FILING DATE: 2004-02-10
FRIOR APPLICATION NUMBER: US 60/446,730
PRIOR FILING DATE: 2003-02-10
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 71, Application US/60248592; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Rattus norvegicus
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CRGANISM: HUMAN
US-60-248-592-71
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US-10-775-481A-55
                                               PCT-US04-03765-55
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LENGTH: 111
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GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
APPLICANT: Beasley, Ellen
TITLE OF INVENTION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/245,228
CURRENT PILING DATE: 2000-11-03
NUMBER OF EQ ID NOS: 630
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 122
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                                                                                                                                            7 SGLLTGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAV 66
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65.3%; Score 358; DB 37; Length 111; 65.7%; Pred. No. 2.2e-32; ive 14; Mismatches 22; Indels
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                                                                                                                                                                                                                                           62 CYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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APPLICANT: Pitari, Giovanni Mario
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
APPLICANT: Schulz, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Lubbe, Wilhelm
TITLE REPERENCE: 08321-168 PC1
CURRENT APPLICATION NUMBER: PCT/USO4/03765
CURRENT FILING DATE: 2004-02-10
PRIOR FILING DATE: 2003-02-10
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PSESEE for Windows Version 4.0
SEG ID NO 56
LENGTH: 112
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  Query Match
Best Local Similarity 65.74
Matches 69; Conservative
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ORGANISM: Homo sapiens
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DEPLICANT: Cetin, Yalcin
APPLICANT: Savas, Yuksel
TITLE OF INVENTION: Uselance-cyclase C ligand, administered via the airways, for the
TITLE OF INVENTION: Quanylate-cyclase C ligand, administered via the airways, for the
TITLE OF INVENTION: treatment of respiratory airway problems
FILE REPERENCE: 03100192aa
CURRENT APPLICATION NUMBER: US/10/479,606
CURRENT APPLICATION NUMBER: DEI0127119.0
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.2
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US-10-700-439-145

Sequence 145, Application US/10700439

GENERAL INFORMATION:

APPLICANT: Bayer Healthcare LLC

APPLICANT: Bayer Healthcare LLC

APPLICANT: Bayer Healthcare LLC

APPLICANT: Thiagalingam, Arunthathi

APPLICANT: Thiagalingam, Arunthathi

APPLICANT: Thiagalingam, Arunthathi

APPLICANT: Thiagalingam, Arunthathi

APPLICANT: Thiagalingam, Steven

APPLICANT: Boardman, Lisa A.

APPLICANT: Thibodeau, Steven

APPLICANT: Thibodeau, Steven

APPLICANT: Thibodeau, Steven

APPLICANT: Lewis, Marcia

TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as TITLE OF INVENTION: Biomarkers for Cancer

TITLE OF INVENTION: Biomarkers for Cancer

TITLE OF INVENTION: Biomarkers 105/10022

CURRENT FILING DATE: 2003-11-04

NUMBER OF SEQ ID NOS: 186

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 145

LENGTH: 112
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                                                                                                                        62 CYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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                                                                                                                                                                                                                                      US-10-479-606-5; Sequence 5, Application US/10479606; GENERAL INFORMATION:
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CORGANISM: homo sapiens
US-10-479-606-5
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ORGANISM: Homo sapiens
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LENGTH: 112
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Sequence 19134, Application US/10170205E

GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170, 205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 19124
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leads, Marcia
TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
TITLE OF INVENTION: Biomarkers for Cancer
TITLE REFERENCE: 1657/2022
CURRENT APPLICATION UNBER: PCT/US04/36404
CURRENT FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 1864-11-09
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 145
LENGTH: 112
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                    2 SGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDV 61
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: Bayer Healthcare LLC APPLICANT: Burgess, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
65.0%; Score 356; DB 1; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels
                                                                                                                62 CYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
                                                                                                                                            62 CYNPALPLDLOPYCASOBAASTFKALRTIATDECELCINVACTGC 106
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                                                                                                                                                                                                                                                          PCT-US04-36404-145; Sequence 145, Application PC/TUS0436404; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Myerow, Susan
Thiagalingam, Arunthathi
Maimonis, Peter
Molino, Gary
Burgart, Lawrence
Boardman, Lisa A.
Thibodeau, Steven
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-170-205E-19124
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US-10-170-205E-19124
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, MAY
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1457;
CURRENT FILING DATE: 2003-03-10
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FRRESC for Windows Version 4.0
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ch 65.0%; Score 356; DB 33; Length 112; Similarity 65.7%; Pred. No. 3.8e-32; 69; Conservative 14; Mismatches 22; Indels
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65.7%; Pred. No. 3.8e-32;
iive 14; Mismatches 22; Indels
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                                                                                                                                                             62 CYNPALPLDLOPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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65.0%; Score 356; DB 37;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22;
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US-10-775-481A-56

Sequence S6, Application US/1075481A

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Jason
APPLICANT: Britari, Giovanni Mario
APPLICANT: Britari, Stephanie
APPLICANT: Schulz, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Unbbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08221-0168 US1
CURRENT APPLICATION NUMBER: US/10/775,481A
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/446,730
PRIOR APPLICATION DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOSTWARE: FRASEEQ for Windows Version 4.0
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US-60-453-050-12227
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Query Match
Best Local Similarity
Matches 69; Conserv
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Best Local Similarity
Matches 69; Conserv
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US-60-453-050-12227
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LENGTH: 112
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LENGTH: 112
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: TAXCOBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT PILING DATE: 2003-031-0
NUMBER OF SEQ ID NOS: 82762
SEQ ID NO 12227
LENGTH: 112
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF ENQ ID NOS: 429241
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 12227
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                             7 SGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAV 66
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2 SGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDV
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                                                                                                                                            67 CHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGC 111
                                                                                                              62 CYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22;
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67.5%; Pred. No. 1.7e-26;
tive 12; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26398, Application US/09834366
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Johert, Severin
APPLICANT: Johert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: 81.USZ-REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT APPLICATION NUMBER: US 60/197,873
FRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 26398
LENGTH: 93
                                   Sequence 1020, Application US/60568073
GENERAL INFORMATION:
APPLICANT: Huang, Fei
APPLICANT: Han, Xia
APPLICANT: Shaw, Peter
APPLICANT: Clark, Edwin
TITLE OF INVENTION: COLON CANCER BIOMARKERS
FILE REFERENCE: 10205 PSP
CURRENT FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 1305
SOFTWARE: PatentIn version 3.2
LENGTH: 112
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Best Local Similarity 67.5<sup>§</sup>
Matches 56; Conservative
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CORGANISM: Homo sapiens
US-60-568-073-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-834-366-26398
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RESULT 14
US-60-568-073-1020
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Search completed: March 26, 2005, 17:10:17 Job time : 437.927 secs

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Query Match
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Sequence 1382, Ap
Sequence 1384, Ap
Sequence 169824,
Sequence 162948,
Sequence 16594,
Sequence 161554,
Sequence 161177,
Sequence 161177,
Sequence 161177,
Sequence 16290,
Sequence 1629, Ap
Sequence 41944, A
Sequence 41944, A
Sequence 41544, A
Sequence 2766, Ap
Sequence 2766, Ap
Sequence 13880, A
Sequence 36811, A
Sequence 36811, A
Sequence 36811, A
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1, Appli
39, Appl
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165482,
                                                           March 26, 2005, 16:44:35 ; Search time 32.8832 Seconds (without alignments) 187.395 Million cell updates/sec
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                                                                                                     US-10-775-481A-55
548
1 MSGSQLWAAVLLLUVLQSAQ.......LRTIATDECELCINVACTGC 106
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1: /cgn2_6/ptodats/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodats/1/paa/US07_NEW_COMB.pep:*

3: /cgn2_6/ptodats/1/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodats/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodats/1/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodats/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodats/1/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodats/1/paa/US11_NEW_COMB.pep:*
5.1.6
Compugen Ltd
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PCT-USO4-42360-1382
US-60-655-875-169824
US-60-655-875-169824
US-10-450-763-334297
US-60-655-875-161177
US-60-655-875-161177
US-60-655-875-161177
US-10-450-763-3125
US-10-450-763-3126
US-10-450-763-3126
US-11-450-763-31880
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US-10-436-715A-69
US-60-655-875-165482
US-10-450-763-57226
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                               260697 segs, 58133403 residues
GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 168716,
Sequence 10987, A
Sequence 1428, Ap
Sequence 1428, Ap
Sequence 53050, A
Sequence 53052, A
Sequence 44, Appl
Sequence 150648,
Sequence 136, Appl
Sequence 136, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 54287, Sequence 54287, Appli
Sequence 54287, Appli
Sequence 54287, Appli
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31187, A
56918, A
31174, A
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US-60-643-717-9245

US-11-031-175-12044

US-60-655-875-162823

US-60-655-875-168716

US-11-031-175-10987

PCT-USO4-17965-1428

PCT-USO4-17965-1428

US-10-450-763-4468

US-10-450-763-53050

PCT-USO5-01469-44

US-10-450-763-53052

US-10-450-763-53052

US-10-450-763-5064

US-11-021-911-36

US-11-021-911-36

US-11-021-911-36

US-11-450-763-40066

US-11-450-763-4187

US-10-450-763-1187

US-10-450-763-1187

US-10-450-763-1187
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ALIGNMENTS

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RESULT 2
PCT-US05-03483-6
; Sequence 6, Application PC/TUS0503483
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MANZAS AS MODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE;
; FILE REPERENCE: EX05-005
NESULT 1
US-11-066-697-1249

Sequence 1249

Sequence 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-11-066-697-1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 81; DB 7; Length 16.85.7%; Pred. No. 0.0043; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 DECELCINVACTGC 106
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Matches 12; Conserv
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OTHER INFORMATION: Homolog annotation: Hit_ID=NP_506153.1; Match level="QueryCoverage OTHER INFORMATION: =97%, HitCoverage=10%, E-value=90-30, Identity=37%", Hit descripting OTHER INFORMATION: =TEMO (5N87) [Caenorhabditis elegans] emb|CAA98425.1| Hypothetical|OTHER INFORMATION: protein C14C10.5 [Caenorhabditis elegans] emb|CAA98425.1| Figothetical|PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_96247; Strand=+; Position=2-(
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21 (53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 169824
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QLWAAVLLLLVLQSAQG-----VYIKYHGFQVQLESVKKLNELEEKQMSDPQQQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Gaps
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                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                           Length 1959,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 68; DB 8; Length 201; 23.7%; Pred. No. 3.2; tive 17; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                     49 DPOQOKSGLLPDVCYNPALPLDLOPVCASQEAASTFKALRTIATDECE
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                           DB 1;
                                                                                             TYPE: PRT
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: SWISS-Prot / M64780
DATABASE ENTRY DATE: 2003-02-28
                                                                                                                                                                                                                                                        ; Score 69.5; DB
; Pred. No. 36;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 169824, Application US/60655875 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Heterodera glycines
                                                                                                                                                                                                                                                      Query Match 12.7%;
Best Local Similarity 26.2%;
Matches 21; Conservative 7
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Guo, Liang
Kovalic, David
Lu, Maolong
McCarter, James
Miller, Nancy
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Vaudin, Mark
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Matches 27, Conservative
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 1384
LENGTH: 1959
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US-60-655-875-162848
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US-60-655-875-169824
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APPLICANT:
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Sequence 1382. Application PC/TUSO442360

Sequence 1382. Application PC/TUSO442360

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation doing business as Massachusetts General

APPLICANT: The General Hospital / Bayer AG

TITLE OF INVENTION NUCLECTION SET 17633/2048

CURRENT FILING DATE: 2004-12-17

PRIOR APPLICATION NUMBER: 60/531,341

PRIOR APPLICATION NUMBER: 60/531,341

PRIOR APPLICATION NUMBER: 60/531,341

SEC ID NOS: 2587

SOFTWARE: PELI SCRIPT

SEQ ID NO 1382

LENGTH: 1959
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: 60/531,341
PRIOR APPLICATION NUMBER: 60/531,341
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                                                                                                                                                                                                                                                                                   Score 73; DB 1; Length 1139;
Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 DPQQQKSGLLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATDECEL
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PUBLICATION INFORMATION:
DATMBASE ACCESSION UNMBER: SWISS-Prot / M64780
DATABASE ENTRY DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.7%; Score 69.5; D
Best Local Similarity 26.2%; Pred. No. 36;
Matches 21; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                  17; Mismatches
         CURRENT APPLICATION NUMBER: PCT/USOS/03483
CURRENT FILING DATE: 2005-01-27
PRIOR APPLICATION NUMBER: US60/539,837
PRIOR FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 ----- 104
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833 CVSLKALSSQRWLRTMST 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 CASQEAASTFKALRTIAT 92
                                                                                                                                                                                                                                                                                       Query Match 13.3%;
Best Local Similarity 29.5%;
                                                                                                                                                                                                                                                                                                                                       23; Conservative
                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US04-42360-1384
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                                                                                                                                                                            LENGTH: 1139
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FEATURE:
OTHER INFORMATION: Homolog annotation: Hit_ID=CAE60769.1; Match level="QueryCoverage OTHER INFORMATION: =100%, HitCoverage=66%, E-value=6e-80, Identity=64%"; Hit descrip OTHER INFORMATION: Hypothetical protein CBG04457 [Caenorhabditis briggsae]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_87977; Strand=+; Position=3-
US-60-655-875-161554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER INFORMATION: Gene Ontology: Mol. function=protein binding; Cellular component
OTHER INFORMATION: =cytoplasm; Biological process=protein folding
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vaudin, Mark

APPLICANT: Vaudin, Mark

JITLE OF INVENTION: MI PLANTS AND COMPOSITIONS THEREOF

FILE REPERENCE: 38-21(53885)

CURRENT APPLICANTION NUMBER: US/60/655,875

CURRENT FILING DATE: 2005-02-24

NUMBER OF SEQ ID NOS: 171306

LENGTH: 212

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.0%; Score 65.5; DB 8; Length 212; Best Local Similarity 27.2%; Pred. No. 6.6; Matches 22; Conservative 10; Mismatches 34; Indels 15;
                                                                      ----ALGSALÓGPAQVŚWPQLLŚTYRLLHSL 185
61 VCYNPALPLDLQ-PVCAS-QEAASTFKALRTI
                                                                                                                                                                                                                                                              Sequence 161554, Application US/60655875 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Heterodera glycines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Boukharov, Andrey
APPLICANT: Du, Zijing
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maclong
APPLICANT: MCCarter, James
APPLICANT: Miller, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                           Guo, Liang
Kovalic, David
Lu, Maolong
McCarter, James
Miller, Nancy
Williams, Deryck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boukharov, Andrey APPLICANT: Du, Zijing
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OTHER INFORMATION: Homolog annotation: Hit ID=NP_506153.1; Match level="QueryCoverag OTHER INFORMATION: =99%, HitCoverage=15%, \overage=15, \overage=15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_89271; Strand=+; Position=2-
US-60-655-875-162848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
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                                                                                                                                                                                                                                                                              APPLICANT: Vaudin, Mark
APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 162848
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QLWAAVLLLIVLQSAQG-----VYIKYHGFQVQLESVKKLNELEEKQMSDPQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 KSGLLPDVCYNPALPL-DLQPVCASQEAASTF------KALRTIATDE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.4%; Score 68; DB 8; Length 295; Best Local Similarity 23.7%; Pred. No. 5.1; Matches 27; Conservative 17; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## APPLICATE: Hyear, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER: OF SEQ ID NOS: 60736
SOFTWARE: Cuecom
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32.6%; Pred. No. 5.2;
tive 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34297, Application US/10450763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Heterodera glycines
                                                              Guo, Liang
Kovalic, David
Lu, Maolong
McCarter, James
Miller, Nancy
Williams, Deryck
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Best Local Similarity 32.6
Matches 30; Conservative
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                               Du, Zijing
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                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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ORGANISM:
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10 VLLLLVLQSAQG-----VYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDVC 62
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PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2000-00-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR PELING DATE: 2000-02-30
PRIOR PILING DATE: 2000-02-30
PRIOR PILING DATE: 2000-02-30
PRIOR PELING DATE: 2000-02-30
PRIOR PELING DATE: 2000-02-20
PRIOR PELING DATE: 2000-02-20
PRIOR PELING DATE: 2000-02-20
PRIOR PILING DATE: 2000-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/489,448 CURRENT FILING DATE: 1004-03-10
                                                                                                                                                                                                      Sequence 1225, Application US/10489448
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
                                    182 AACFIKLMEFQRAVDDCDLCL 202
      81 ASTFKALRTI -- ATDECELCI 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weng, Gezhi
Haley-Vicente, Dana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou, Ping
Ghosh, Malabika
Wang, Dunrui
Ma, Yunqing
Asundi, Vinod
                                                                                                                                                                                                                                                               Tang, Y. Tom
Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Wehrman, Tom
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Best Local Similarity 31.6
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1225
                                                                                                                                                     RESULT 11
US-10-489-448-1225
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                                                                                                                                                                          OTHER INFORMATION: Homolog annotation: Hit_ID=CAE60769.1; Match level="QueryCoverage OTHER INFORMATION: =100%, HitCoverage=68%, E-value=5e-83, Identity=64%"; Hit descrip OTHER INFORMATION: Hypothetical protein CBG04457 [Caenorhabditis briggsae]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Homolog annotation: Hit ID=CAE60769.1; Match level="QueryCoverage OTHER INFORMATION: =99%, HitCoverage=84%, E-value=1e-101, Identity=62%"; Hit descrip OTHER INFORMATION: Hypothetical protein CBG04457 (Caenorhabditis briggsae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
, OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_89323; Strand=+; Position=84
US-60-655-875-162900
                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_87600; Strand=+; Position=1-
US-60-655-875-161177
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Gene Ontology: Mol. function=protein binding; Cellular component OTHER INFORMATION: =cytoplasm; Biological process=protein folding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Gene Ontology: Mol. function=UDP-N-acetylglucosamine-peptide N OTHER INFORMATION: -acetylglucosaminyltransferase activity; Cellular component OTHER INFORMATION: -perinuclear space; Biological process=protein folding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Waudin, Mark

APPLICANT: Wu Wei

TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF

FILE REFERENCE: 38-21 (5388): US/60/655,875

CURRENT APPLICATION NUMBER: US/60/655,875

CURRENT FILING DATE: 2005-02-24

NUMBER OF SEQ ID NOS: 171306

LENGTH: 271

TYPE: ...

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 65.5; DB 8; Length 218; 27.2%; Pred. No. 6.8; tive 10; Mismatches 34; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 65.5; DB 8; Length 271; llarity 27.2%; Pred. No. 9; Conservative 10; Mismatches 34; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ASTFKALRTI -- ATDECELCI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Heterodera glycines
                                                                                                                   ORGANISM: Heterodera glycines
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 161177
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boukharov, Andrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Du, Zijing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity. Matches 22; Conserva
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Best Local Similarity
Matches 22; Conserv
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US-60-655-875-162900
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LOCATION: (896)...(941)
OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
OTHER INFORMATION: 13.17
                                                                                                                             54
                                                                                               2 SGSQLWAA------VLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SGSQLWAA------VLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQK
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                       55 SGLLPDVCYNPALPLDLQPVCASQEAASTFKA-----LRTIATDECELCINVA 102
                                                                                                                                                                                                                 55 SGLLPDVCYNPALPLDLQPVCASQEAASTFKA-----LRTIATDECELCINVA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
           DB 6; Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 64.5; DB 6; Length 1307; 22.8%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                               GENERAL LINGUISTICS.

J STRICK ALL MENOMENTION:

J TILE REFERENCE: 790(CTB2/US

FILLE REFERENCE: 790(CTB2/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR FILING DATE: 2003-06-11

PRIOR FILING DATE: 2001-03-30

PRIOR PLING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 41544

LENGTH: 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERBNCE: 38-21(53629)A
CURRENT APPLICATION UNWBER: US/60/643,717
CURRENT FILING DATE: 2005-01-12
SEQ ID NOS: 19247
LENGTH: 331
                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 8;
Pred. No. 17;
         11.8%; Score 64.5; D 22.8%; Pred. No. 76; ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Crocosphaera watsonii WH 8501
US-60-643-717-2766
                                                                                                                                                                                                                                                                                                                                              Sequence 41544, Application US/10450763 GENERAL INFORMATION:
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25.0%;
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                                                       Conservative
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                              Best Local Similarity
Matches .26; Conserv
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      Query Match
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OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
OTHER INFORMATION: 13.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (91)..(204)
OTHER INFORMATION: ZAP domain identified by PFam, accession name ZAP, E-value=
OTHER INFORMATION: 6.3e-19, PFam score of 76.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 YIKYHGFQVQLESVKKLNE-----LEEKQMSDPQQQKSGLLPDVCYNPALPLDLQPVCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                              FILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%; Score 65; DB 6; Length 341;
22.7%; Pred. No. 14;
ive 21; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : LOCATION: (1) ... (1225)
; OTHER INFORMATION: Xaa = X or * as defined in Table US-10-450-763-41984
US-10-450-763-36316; Sequence 36316, Application US/10450763; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41984, Application US/10450763 GENERAL INFORMATION:
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206 TDQATSDFQLMKAVA 220
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NAME/KEY: misc_feature
LOCATION: (1)...(1225)
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 36316
LENGTH: 341
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Matches 21; Conservative 14; Mismatches 35; Indels 14; Gaps 4;

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77 SOEAASTFKALRTIATDECELCIN 100

Search completed: March 26, 2005, 17:11:53 Job time : 32.8832 secs

Sequence 145, App Sequence 19124, A Sequence 5, Appli

Description

DB

Length

Seguence:

Run on:

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Query
Match
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216
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579
1 MGCRAASGLLPGVAVVLLLL......RTIANDDCELCVNVACTGCL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pending Patents AA Main:*

1: \(\cggn2_6\)\ptodata/1/\paa/US06_COMB.pep:*

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5: \(\cgn2_6\)\ptodata/1/\paa/US08_COMB.pep:*

6: \(\cgn2_6\)\ptodata/1/\paa/US08_COMB.pep:*

6: \(\cgn2_6\)\ptodata/1/\paa/US08_COMB.pep:*

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12: \(\cgn2_6\)\ptodata/1/\paa/US08_COMB.pep:*

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19: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

10: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

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21: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

22: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

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24: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

25: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

26: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

27: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

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20: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

21: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

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23: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

24: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

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28: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

29: \(\cgn2_6\)\ptodata/1/\paa/US09_COMB.pep:*

20: \(\cgn2_
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6/ptodata/l/paa/US104_COMB.pep:
6/ptodata/l/paa/US105_COMB.pep:*
6/ptodata/l/paa/US106_COMB.pep:*
6/ptodata/l/paa/US107_COMB.pep:*
-/nrodata/l/paa/US108_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6959266 seqs, 1168006243 residues
                                                                                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Database

Sequence 145, App Sequence 167, App Sequence 1227, A Sequence 1227, A Sequence 1227, A Sequence 1227, A Sequence 23, Appl Sequence 25, Appl Sequence 157, App Sequence 157, App Sequence 157, App Sequence 1711, Appl Sequence 12, Appl Sequence 1228, A Sequence 1238, A Seq

PCT-US04-03765-56

PCT-US04-3644-145

US-10-17-0205E-19124

US-10-17-0205E-19124

US-10-17-04145-145

US-10-17-0414-145

US-10-775-481A-56

US-60-453-050-1227

US-60-453-135-1227

US-60-453-135-1227

US-60-453-135-1227

US-60-453-135-1227

US-60-17-481A-55

US-60-17-481A-55

US-60-17-481A-55

US-60-17-481A-55

US-60-17-67-69

US-10-17-67-190

US-10-17-67-17-190

US-10-17-17-190

US-10-262-473-16

US-10-262-473-16

US-10-262-473-17

US-60-453-135-171

US-60-453-135-171

US-60-453-135-171

US-60-453-135-171

US-60-473-14

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1	Sequence 56, Application PC/TUS0403765	; GENERAL INFORMATION: ; APPLICANT: Waldman, Scott A.	; APPLICANT: Pitari, Giovanni Mario	, APPLICANT: Schulz, Stephanie	; APPLICANT: Lubbe, Wilhelm	; TITLE OF INVENTION: The Use Of GCC Ligands	; FILE REFERENCE: 08321-168 PC1	; CURRENT APPLICATION NUMBER: PCT/US04/03765	; CURRENT FILING DATE: 2004-02-10	, PRIOR APPLICATION NUMBER: US 60/446,730	; PRIOR FILING DATE: 2003-02-10	, NUMBER OF SEQ ID NOS: 56	; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ ID NO 56

Sequence 14, Appl Sequence 78, Appl Sequence 4187, Ap Sequence 6139, Ap Sequence 613, Ap

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Query Match
Best Local Similarity 100.0
Matches 112; Conservative
                                                                                                 Query Match
Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: homo sapiens
US-10-479-606-5
TYPE: PRT
ORGANISM: Homo sapiens
                                   ; OKGANISM: DOWO SC
US-10-170-205E-19124
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001341
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 19124
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
APPLICANT: Lewis, Marcia
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
TITLE OF INVENTION: Bload Los Cancer
FILE REFERENCE: 1657/2022
FILE REFERENCE: 1657/2022
CURRENT APPLICATION VMBER: PCT/US04/36404
CURRENT FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 60
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                                                                                                                                                                                                                         1 MGCRAASGLLPGVAVVLLLLLQSTQSVY1QYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 60
                                                                                                                                                                                                                                                             1 MGCRAASGLLFGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 60
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                                                                                                                          Query Match 100.0%; Score 579; DB 1; Length 112; Best Local Similarity 100.0%; Pred. No. 7e-56; Matches 112; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education and Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 19124, Application US/10170205E; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145, Application PC/TUS0436404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgess, Christopher
Myerow, Susan
Thiagalingam, Arunthathi
Maimonis, Peter
Molino, Gary
Burgart, Lawrence
Boardman, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bayer Healthcare LLC
                              TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US04-36404-145
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US-10-170-205E-19124
                                                                            PCT-US04-03765-56
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LENGTH: 112
       LENGTH: 112
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APPLICANT:
APPLICANT:
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Sequence 5. Application US/10479606
Sequence 5. Application US/10479606
GENERAL INFORMATION:
APPLICANT: Cetin, Yalcin
APPLICANT: Savas, Yukas
APPLICANTON: Creatment of respiratory airway problems
TITLE OF INVENTION: Creatment of respiratory airway problems
TITLE OF INVENTION: Creatment of respiratory airway problems
TITLE OF INVENTION: USBERS 105/10/479,606
CURRENT FILING DATE: 2003-12-04
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/DE02/02040
PRIOR APPLICATION NUMBER: PCT/DE02/02040
PRIOR APPLICATION NUMBER: PCT/DE02/02-06-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Version 3.2
SOFTWARE: PatentIn Version 3.2
SOFTWARE: PatentIn Version 3.2
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APPLICANT: Boardman, Lisa A.
APPLICANT: Boardman, Lisa A.
APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
TITLE OF INVENTION: Blomarkers for Cancer
FILE REPRENCE: 1657/2022
CURRENT APPLICATION NUMBER: US/10/700,439
CURRENT FILING DATE: 2003-11-04
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100.0%; Score 579; DB 27; Length 112; 100.0%; Pred. No. 7e-56; ive 0; Mismatches 0; Indels 0;
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100.0%; Pred. No. 7e-56;
ive 0; Mismatches 0; Indels 0.
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GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: Bayer Healthcare LLC
APPLICANT: Burgess, Christopher
APPLICANT: Myerow, Susan
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Maimonis, Peter
Molino, Gary
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-12227
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, MAP
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01457
; CURRENT PELLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FBSLSEQ for Windows Version 4.0
; SEQ ID NO 12227
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                                                                                                                                                           DB 33;
                                                                                                                                                           Score 579; DB 33
Pred. No. 7e-56;
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100.0%; Pred. No. 7e-56;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Waldman, Scott A.
APPLICANT: Picari, Giovanni Mario
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
APPLICANT: Schulz, Stephanie
APPLICANT: Lubbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-0168 USI
CURRENT APPLICATION NUMBER: US/10/775,481A
CURRENT APPLICATION NUMBER: US 60/446,730
PRIOR PILING DATE: 2003-02-10
PRIOR PILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 56
                                                                                                                                                                                                0; Mismatches
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145
LENGTH: 112
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Best Local Similarity 100.
Matches 112; Conservative
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Best Local Similarity 100.
Matches 112; Conservative
                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-700-439-145
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ORGANISM: Homo sapiens
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US-60-453-050-12227
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US-60-453-135-1227
US-60-453-135-1227
US-60-453-135-1227
Sequence 1227, Application US/60453135
Sequence 1227, Application US/60453135
Sequence 1227, Application US/60453135
APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: MYCCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WHOSER: US/60/453,135
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT PILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12227
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF ESQ ID NOS: 429241
SOFTWARE: FREEEEQ for Windows Version 4.0
SEQ ID NO 12227
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; Score 579; DB 37; Length 112; ; Pred. No. 7e-56; 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 7e-56;
tive 0; Mismatches 0;
     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 112; Conservative 0
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Best Local Similarity 100.
Matches 112; Conservative
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US-60-466-412-12227
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US-60-453-135-12227
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US-09-834-366-26398
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SEQ ID NO 71
LENGTH: 111
                        US-60-248-592-71
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GENERAL INFORMATION:
APPLICANT: Beasley. Ellen
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOO878
CURRENT APPLICATION NUMBER: US/60/245,228
CURRENT PILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 630
SOFTWARE: FastSEQ for Windows Version 4.0
1 MGCRAASGILPGVAVVLILILQSTQSVYIQYQGFRVQLESMKKLSDIEAQWAPSPRLQAQ 60
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0; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Huang, Fei
APPLICANT: Hang, Kiei
APPLICANT: Ghaw, Peter
APPLICANT: Grak, Edwin
TITLE OF INVENTION: COLON CANCER BIOMARKERS
FILE REFERENCE: 10205 PSP
CURRENT APPLICATION NUMBER: US/60/568,073
CURRENT FILING DATE: 2004-05-04
NUMBER OF ESQ ID NOS: 1305
SOFTWARE: Patentin version 3.2
FEQUIN 0.1020
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Matches 112, Conservative
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Best Local Similarity 99.1
Matches 111; Conservative
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ORGANISM: HUMAN
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US-60-245-228-223
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SEQ ID NO 223
LENGTH: 122
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Sequence 71, Application US/60248592
GENERAL INFORMATION:
BAPELICAMY: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/248,592
CURRENT APPLICATION NUMBER: 2000-11-16
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FRANCE FARENCE FOR Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCRAASGLLTGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 OSTOSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26398, Application US/09834366; GENERAL INPORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENITON: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.U32.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT APPLICATION NUMBER: 01.03.
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.9%; Score 567; DB 37; Best Local Similarity 99.1%; Pred. No. 1.5e-54; Matches 110; Conservative 0; Mismatches 1;
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US-60-197-873-26398
Sequence 26398, Application US/60197873
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
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CORGANISM: Homo sapiens
US-09-834-366-26398
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 SGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SGSQLWAAVLLILVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5%; Score 356; DB 1; Length 106; Best Local Similarity 65.7%; Pred. No. 5.2e-31; Matches 69; Conservative 14; Mismatches 22; Indels
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
PAPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TILLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.03. PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT PILING DATE: 2000-04-18
CURRENT FILING DATE: 2000-04-18
SOFTWARE: Patent.pm
SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 26398
TENGTH: 93
TYPE: PROMO SABJENG
ORGANISM: Homo sapiens
US-60-197-873-26398
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GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Giovanni Mario
APPLICANT: Pitari, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Wolfe, Henry R.
TILE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-168 PC1
CURRENT FILING DATE: 2004-02-10
FRIOR APPLICATION NUMBER: PC7/US04/03765
CURRENT FILING DATE: 2004-02-10
FRIOR APPLICATION NUMBER: US 60/446,730
FRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 106
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CRGANISM: Rattus norvegicus
PCT-US04-03765-55
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Search completed: March 26, 2005, 17:10:18 Job time : 463.715 secs This Page Blank (Uspto)

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WESULT 1

US-11-066-697-1249

Sequence 1249

GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Deminique P.
APPLICANT: Alan M.
APPLICANT: Thibaudeau, Raren
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPONENTS
FILE REPREEMENTS: SOOGS-202301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT PILING DATE: 2005-02-25
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1249
LEWING HILL VER. 2.1
                                                           Sequence 58, Appl
Sequence 5139, Ap
Sequence 50350, A
Sequence 41255, A
Sequence 1190, Ap
Sequence 1190, Ap
Sequence 43513, A
Sequence 146849,
Sequence 56461,
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Sequence 90, Appl
Sequence 1284, Ap
Sequence 146820,
Sequence 37251, A
                                             131740,
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                  Sequence
Sequence
Sequence
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OTHER INFORMATION: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-10-450-763-47493
; Sequence 47493, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyear, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
US-10-450-763-58595

US-10-489-444-5865

US-10-489-444-58465

US-10-491-5458-58

US-10-499-4519

US-10-499-4519

US-10-499-445-1519

US-10-450-763-41255

PCT-USO4-17965-1190

PCT-USO4-17965-1190

US-10-450-763-43513

US-60-635-875-146849

US-10-450-763-56461

US-10-450-763-56461

US-10-450-763-56461

US-10-450-763-56461

US-10-450-763-56461

US-10-55-345-158868

PCT-USO5-01983-90

US-10-26-34-1284

US-60-655-875-14884

US-60-655-875-14884

US-60-655-875-14884

US-60-655-875-14884
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Matches 16; Conserv
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 62.5
62.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33083, A Sequence 157, App Sequence 29, Appl Sequence 31, Appl Sequence 46026, Sequence 46026, A Sequence 15516, A
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14681, A
236, App
409, App
1493, Ap
52765, A
312, App
36280, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105, App
                                                                                                  March 26, 2005, 16:44:35 ; Search time 34.7445 Seconds
(without alignments)
187.395 Million cell updates/sec
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579
1 MGCRAASGLLPGVAVVLLLL......RTIANDDCELCVNVACTGCL 112
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Sequence 1
Sequence 5
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
          version 5.1.6
- 2005 Compugen Ltd
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US-10-450-763-47493

US-10-450-763-33083

PCT-USO4-31036-29

PCT-USO4-31036-31

US-60-655-875-165482

US-10-46026

US-11-031-175-15516

US-11-031-175-15616

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-14681

US-11-031-175-175-1681

US-10-450-763-52765

US-10-450-763-52765

US-10-450-763-52764

US-10-450-763-31580

US-10-450-763-31580

US-10-450-763-31580

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US-10-450-763-38524
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                                                                                                                                                                                                                                                                     260697 segs, 58133403 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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Match ]
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Bed
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Maximum DB
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41 MKKLSDLEAQWAPSPRLQAQSLLPAVCHHPAL--PQDLQPVCASQEASSIFKTLRTIAND 98
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Best Local Similarity 28.0%; Pred. No. 3.4;
Matches 26; Conservative 12; Mismatches 28; Indels 27; Gaps
                                                                                                                                                                                  APPLICANT: PLEXXIKON, INC.
TITLE OF INVENTION: WOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REPERRNCE: 039363-1793
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR PILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATCHIN VET. 3.2
SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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APPLICANT: Jennifer McIntire
TITLE OF INVENTION: IMMUNE DISEASE
FILE REFERENCE: STAN-23SCIP
CURRENT PLINGE STAN-23SCIP
CURRENT FILING DATE: 2004-09-15
PRIOR PLINGE DATE: 2004-09-15
PRIOR PLINGE DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2002-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Mammalian

OTHER INFORMATION: protein sequence

PCT-USUR-30360-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 73; DB 1; Length 351; 32.0%; Pred. No. 2.7; tive 16; Mismatches 25; Indels
  398 PLNPCPNMHKAPRACAVSALRVLCTHPPTSAGLSPNCSHLQLSS 441
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                               RESULT 4
PCT-US04-30360-157
; Sequence 157, Application PC/TUS0430360
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 29, Application PC/TUS0431036; GENERAL INFORMATION: , APPLICANT: Dale Umetsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(301)
; OTHER INFORMATION: TIM-3, allele 1
PCT-US04-31036-29
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329 ELELPENIADSSCTG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.0%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US04-31036-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (653)...(684)
OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=1.857e-16, raw OTHER INFORMATION: score of 18.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: DOMAIN
LOCATION: (521)...(794)
OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam,
OTHER INFORMATION: accession name pkinase, E-value=1e-68, PFam score of 241.7
US-10-450-763-47493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGTVPRI-----LLQNPRGMDAHSHGTLSFRSQPRTRSGLSQ-EGLWGPARDRYCSHVP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GVAVVILLILLQSTQSVYIQYQGFRVQLESM------KKLSDLEAQWAPSPRLQAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..... 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 GIACARFI---GNRTVÝMESLHMQGEIENQITAAFTMIGTSSHĽSDKCSÓFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVAC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGLLPGVAVVLLLLLQSTQSVYIQYQG---FRVQLESMKKLSDLEAQWAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.9%; Score 74.5; DB 6; Length 985; Best Local Similarity 24.1%; Pred. No. 6.4; Matches 26; Conservative 20; Mismatches 29; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SPRLQAQSLLPAVCHHPALPQDLQPVCASQEASS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-450-763-33083
Sequence 33083, Application US/10450763
SEQUENCE THOROMATION:
SEQUENCE THOROMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
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12.8%; Score 74; DB 6
Best Local Similarity 26.9%; Pred. No. 3.1;
Matches 28; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/USO1/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 33083
LENGTH: 483
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FLING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUBECM
LENGTH: 985
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; ORGANISM: Homo sapiens
US-10-450-763-33083
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TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
   -- EVGQNAYLPCF-YT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LPGVAVVLLLLLQSTQSVYIQYQFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EVGQNAYLPCF-YT 41
                                                                                                                                                  Sequence 31, Application PC/TUS0431036
GENERAL INFORMATION:
APPLICANT: Dale Umecau
APPLICANT: Dale Umecau
APPLICANT: Generale DeKruyff
APPLICANT: Gordon Freeman
TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
TITLE OF INVENTION: IMMURE DISEASE
FILE REFERENCE: STAN-235CIP
CURRENT APPLICATION NUMBER: PCT/US04/31036
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/302,344
PRIOR APPLICATION NUMBER: 10/188,012
PRIOR APPLICATION NUMBER: 10/188,012
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FABSECE for Windows Version 4.0
SEQ ID NO 31
LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALPODLQPVCASQEASSIFK----TLRTIAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 71.5; 28.0%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LUCATION: (1)...(301)
; OTHER INFORMATION: FIM-3, allele 2
PCT-US04-31036-31
   LPFDCVLLLLLLLTRSSEVEYRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarter, James
Miller, Nancy
Williams, Deryck
Vaudin, Mark
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Kovalic, David
Lu, Maolong
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
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US-60-655-875-165482
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LENGTH: 166
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Matches
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; FEATURE:
; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_91905; Strand=+; Position=2-
US-60-655-875-165482
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; OTHER INFORMATION: kw ANNEXIN ANTIGEN PROLINE TUMOR domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM00250A, p-value=6.211e-10, raw score
; OTHER INFORMATION: 10.52
US-10-450-763-46026
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                                                                                                                                                                                                                                                                               48 LOKKKSLHLSFRGTKSTHFSNEREAOKKOPKTHKRRPOTTK--ERDALTKICHAOKLTOO 105
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myscoccue xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/11/031,175
CURRENT APPLICATION NUMBER: 205-01-08
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                                                                                                             Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3N
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                      76 LOPVCASORASS-----IFKTLRTIANDDCELCVNVACTG 110
                                                                                                                                                                                                                                                                                                                                                                                            106 LRRVQSDWESASMVLRRGDAVVVKALR---QDGFSLCDNAVSSG 146
                                                                                                                                                                    Indels
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                                                                                                                                                                    41;
                                                                                                                9,
                                                                                                             <u>DB</u>
                                                                                                          11.8%; Score 68.5; DB
24.0%; Pred. No. 3.6;
tive 19; Mismatches
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11.8%; Score 68.5; DB
Best Local Similarity 31.4%; Pred. No. 47;
Matches 32; Conservative 9; Mismatches
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; Sequence 46026, Application US/10450763
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-10
                                                                                                          Query Match
Best Local Similarity 24.0%
Matches 25; Conservative
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US-10-450-763-49219
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TITLE OF INVENTION: MIGFRS AS MODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE FILE REFERENCE: EXOS-002C-PC CURRENT APPLICATION NUMBER: PCT/USO5/02638
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: US 60/539,837
PRIOR APPLICATION NUMBER: US 60/539,837
PRIOR APPLICATION NUMBER: US 60/552,634
PRIOR APPLICATION NUMBER: US 60/552,634
PRIOR FILING DATE: 2004-03-12
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 120
SOSTWARE PACENTIN VERSION 3.2
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                                                                                                                                                                                                                                                               260 GCRIATGLLGGYVVLYLAFRPMGALADFGRRGDLSYGVYLYAFPVQQAVTTLLGGPTAWW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SGLIPGVAVVLILLLQSTQSVYIQYQGFRVQLESMKKLSDL------EAQM-----A 52
                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                       38 -----LESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEA 85
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: '90CID3'US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                          Query Match
11.7%; Score 68; DB
Best Local Similarity 23.7%; Pred. No. 11;
Matches 27; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 68; DB 23.4%; Pred. No. 50; tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
PCT-USO5-02638-105
; Sequence 105. Application PC/TUS0502638
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 49219, Application US/10450763; GENERAL INFORMATION:
                                                                             ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.4%
Matches 29; Conservative
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
PCT-US05-02638-105
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US-10-450-763-49219
                                                                                                  US-11-031-175-15516
                  SEQ ID NO 15516
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 105
LENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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FEATURE:
NAME/KEY: DOWAIN
LOCATION: (445)...(478)
OTHER INFORMATION: Nuclear hormones receptors DNA-binding region proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00031A, p-value=4.000e-
OTHER INFORMATION: 35, raw score of 19.55
FEATURE:
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (443)...(696)
OTHER INFORMATION: Zinc finger, C4 type (two domains) domain identified by PFa OTHER INFORMATION: accession name zf-C4, E-value=2.3e-57, PFam score of 195.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14681, Application US/11031175

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glater, Steven C.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE REFERENCE: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/11/031,175
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2006-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 KLGSMEDAPARSPRPQDD---PARPQEPTMPPPETPSEGRQPSPSPSPTERAPASEEEFQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 KLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDD--- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RAASGLIPGVAVV-----LLLLLLQSTQSVYIQYQGFR-----VQLESMKKLSDL-EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.7%; Score 67.5; DB 6; Length 819;
Best Local Similarity 27.3%; Pred. No. 31;
Matches 24; Conservative 10; Mismatches 33; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 LAAPSPERVLRAVAMMEQAEVPLRPHLPALLRHP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LPAVCHHP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ----CEL-----CVNVACTGCL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 FLRCQCCQAEAKCPKLLPCLHTLCSGCL 103
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 49219
LENGTH: 819
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 236, Application US/10755415; GENERAL INFORMATION:
APPLICANT: BRAHMACHARI, SAMIR KUMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Myxococcus xanthus
US-11-031-175-14681
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Ghosh, Malabika
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                             APPLICANT: SHARMA, RAMAKANT
APPLICANT: HARMA, RAMAKANT
APPLICANT: MAHESHWART, JITENDRA KUMAR
APPLICANT: MAHESHWART, JITENDRA KUMAR
TITLE OF INVENTION: A COMPUTER BASED VERSATILE METHOD FOR IDENTIFYING PROTEIN CODING
TITLE OF INVENTION: DNA SEQUENCES USEFUL AS DRUG TARGETS
FILE REPERENCE: 026033-00029
CURRENT APPLICATION NUMBER: US/10/755,415
CURRENT PILING DATE: 2003-01-13
PRIOR PELLING DATE: 2003-12-05
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PATENT NOS: 373
SEQ ID NO 236
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PLAMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/11/033,545
CURRENT FILING DATE: 2005-01-12
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PASISEO for Windows Version 4.0
SEQ ID NO 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 OWAPSPR---LOAOSLLPA-----VCHHPALPQDLQPVCASQEASSIFKTLRTI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.6%; Score 67; DB 6; Length 187;
31.0%; Pred. No. 6;
.ive 7; Mismatches 21; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; Score 66.5; DB 7; Length 228; 32.0%; Pred. No. 8.7; tive 12; Mismatches 35; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 HÓAAŚRVPAKGGAPAPSRGPÓELVPTTHPGQPARHPASSV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 -QAQSLLPAVCHHPAL---PQDLQPVC----ASQEASSI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-755-415-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1493, Application US/10489448 GENERAL INFORMATION:
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Best Local Similarity 31.0*
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Conservative
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Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Wehrman, Tom
Zhou, Ping
DEBASIS
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Best Local Similarity
Matches 32; Conserva
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ORGANISM: Human
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US-10-489-448-1493
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APPLICANT:
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APPLICANT:
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APPLICANT:
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242 CEVLKEVIPGVVIETLDLVLET-----PRKSLRGQKMLPLLSQRRFVLLHNGEADP 292
                                                                                                                                                                                                                                        PAPPLICANT: Haley-Vicente, Dana
APPLICANT: Haley-Vicente, Dana
APPLICANT: Haley-Vicente, Dana
APPLICANT: Dirmanac, Radoje T
TITLE OF INVENTION: NOVel Nucleic Acids and
FILE REPERBNCE: 810C1P PCT
CURRENT FILING DATE: 1004-03-10
FRIOR PELION NUMBER: US 60/324,631
FRIOR PLILING DATE: 2000-09-24
FRIOR FILING DATE: 2000-01-21
FRIOR PLILING DATE: 2000-01-21
FRIOR PLILING DATE: 2000-01-22
FRIOR PLILING DATE: 2000-01-22
FRIOR PLILING DATE: 2000-01-22
FRIOR PLILING DATE: 2000-01-22
FRIOR PLILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR PLICATION NUMBER: US 09/496,914
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR PLICATION NUMBER: US 09/560,875
FRIOR FILING DATE: 2000-02-03
FRIOR FILING DATE: 2000-02-05
FRIOR FILING DATE: 2000-02-05
FRIOR PLICATION NUMBER: US 09/515,126
FRIOR FILING DATE: 2000-02-05
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FRIOR FILING DATE: 2000-03-05
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Haley-Vicente, Dana
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Best Local Similarity 24.0<sup>1</sup>
Matches 24; Conservative
Wang, Dunrui
Ma, Yunging
Asundi, Vinod
                                                                                                                      Wang, Zhiwei
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March 26, 2005, 16:49:45; Search time 84.4821 Seconds (without alignments) 86.982 Million cell updates/sec Run on:

US-10-775-481A-2 score:

1 NNTFYCCELCCNPACAGCY 19 Perfect so Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

2105692 segs, 386760381 residues

Searched:

0

Word Bize :

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

A Geneseq 16Dec04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp201s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aar85946 ST Ia rec	Aay40508 ST recept	Adr45822 Amino aci	Adr48355 Immature	Aar85956 ST Ia rec	Aar85950 ST Ia rec	Aay40543 ST recept	Aay40518 ST recept	Aay40512 ST recept	Aay02385 Heat stab	_	Aay02397 Heat stab	В	Adr48332 C. freund	Adr48341 Bacterial	Adr45832 Amino aci	. Adr45857 Amino aci	Adr45826 Amino aci	Aap30262 Sequence	_	Aar85957 ST Ia rec	Aay40519 ST recept	e ST	3 ST	Adr45827 Amino aci
OI	AAR85946	AAY40508	ADR45822	ADR48355	AAR85956	AAR85950	AAY40543	AAY40518	AAY40512	AAY02385	AAY29607	AAY02397	ADR48330	ADR48332	ADR48341	ADR45832	ADR45857	ADR45826	AAP30262	AAR85951	AAR85957	AAY40519	AAY40546	AAY40513	ADR45827
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Query Match	100.0	100.0	100.0	100.0	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	89.5	89.5	89.5	89.5		89.5
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Adr45833 Amino aci Adr45860 Amino aci Adr6671 E. coli h Adr8595 ST Ia rec Adr40514 ST recept Ady40520 ST recept Ady40520 ST recept Adr45828 Amino aci Adr45828 Amino aci Adr45828 ST Ia rec Adr40515 ST recept Ady40521 ST recept Ady40521 ST recept Ady40521 ST recept Ady40521 ST recept Ady40521 ST recept	
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26 27 27 28 30 30 31 31 32 33 34 34 35 36 36 40 40	44444 44321 44321 4432 443

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ALIGNMENTS

RESULT 1

ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer; AAR85946 standard; peptide; 19 AA. ST Is receptor ligand portion. 93US-00141892. 94US-00305056. (UYJE-) UNIV JEFFERSON THOMAS 94WO-US012232. (first entry) colorectal, metastasis. WPI; 1995-178646/23. Escherichia coli. WO9511694-A1. 26-OCT-1994; 26-OCT-1993; 13-SEP-1994; 19-JAN-1996 04-MAY-1995 Waldman SA; AAR85946; AAR85946

Conjugated cpds. which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.

Claim 3; Page 116; 133pp; English.

New conjugated compounds are provided which consist of (1) an ST receptor binding moiety and (2) an active moiety which is a radio- stable agent. 'ST refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate

Sequence 19 AA;

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The specification describes a method for increasing the number of heat stable toxin (ST) receptor molecules on the surface of a metastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 mW of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the commber of ST receptors can then be used to inhibit proliferation of the colorectal, creceptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that have diseases that affect colorectal, gastric and cosophageal cells, including colorectal, gastric or oesophageal cancers.

The present sequence represents a ST, designated ST Ia, which is used as the ST receptor ligand in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer; anorectic; cardiovascular; cytostatic; antiemetic; nespiratory; neburoprotective; vasotropic; auditory; antiemetic; antiasthmatic; nephrotropic; virucide; immunosuppressive; antiallergic; antidabetic; ophthalmological; tranquiliser; hypnotic; nootropic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder; irritable bowel syndrome; constipation; gastrointestinal disorder; hearburn; dyspepsia; gastroparesis; Crohn's disease; incrative colitis; inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.
heat stable toxin; ST, ST receptor; colorectal cancer; gastric cance: oesophageal cancer; colorectal cell; gastric cell; oesophageal cell; ST Ia.
                                                                                                                                                                                                                                                                                                                                                                              Schulz S, Wolfe HR;
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100.0%; Pred. No. 1e-13;
iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                       (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                  10-FEB-2004; 2004WO-US003765.
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Matches 19; Conservative
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                                                                                                                                                           WO2004071436-A2
                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a conjugated compound that comprises a ST (heatstable toxin) receptor moiety selected from one of the sequences shown in ANAVGOSOB-Y40559 and an active moiety (entisense molecule). The compound is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells. The present sequence represents the amino acid sequence of a ST receptor peptide ST la
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
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                                Query Match

100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 19; Conservative 0; Mismatches 0; Indels
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Matches 19; Conservative
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N-PSDB; AAZ07540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
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RESULT 2

AAY40508

AAY40508

AAY

AAC

AAY4

AAC

AAY4

AAC

AAY40508

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BAY40508

BAY406

BAY40

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Gaps

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Length 19; 0; Indels

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The invention relates to a purified peptide (P1) capable of activating the guanylate cyclase C (GC-C) receptor. Further disclosed is a pharaceutical composition comprising the peptide of the invention. The composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastrointestinal disorder; discrete is gastrointestinal motility disorder, considering the plant of the invention is useful for treating gastrointestinal disorder, gastroesophageal reflux disease, functional gastrointestinal disorder, gastroesophageal reflux disease, functional constitution, crohn's disease, ulcerative collitis or inflammantory bowel disease. The peptide of the invention is also useful for treating constitution, crohn's disease, ulcerative collitis or inflammatory bowel conserved to construction, crohn's disease, ulcerative collitis or inflammatory bowel conserved to conserve disease, ulceration is also useful for treating converting the proposition of the invention is also useful for treating converting the conserved disorder. Plantacipation, insulin-related disorder with carbonate imbalance, erectile dysfunction, insulin-related disorder or conserved morphying. Plus useful in relaving symptoms of gastroparesis such as nausea, voniting, bloating, and delayed gastric emptying. Plus useful in relaving symptoms of gastroparesis conserving an englitus, hyperglyceamia, respirating or preventing retinopathy and edems formation. Plus useful for treating or preventing repropathy negatesis, anxiety, aleeg disorders and memory loss. Plus useful as a marker to identify, decet, stage, or diagnosis diseases and conditions of the small intestine, including Ccohn's disease, colitis, inflammatory conserved in trangeting and specific cells bearing doc diagnosis or the conserved collection or lacal colorectal for versating or treating or treating colorectal for intestine to add in imaging and diagnosing or treating colorectal for each or local colorectal for where the specific cells bearing documents
cancer; respiratory disorder; neurological disorder; carbonate imbalance; exectile dysfunction; inner ear disorder; slow digestion; nausea; vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy; retinopathy; nephropathy; nation and an an arxiety; sleep disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a bacterial ST peptide which is an activator of the GC-C
receptor. ST peptides are considered super agonists of GC-C and are very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified peptide capable of activating the guanylate cyclase (receptor, useful for treating obesity, congestive heart failure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistant to proteolytic degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 30; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         benign prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                      15-MAY-2003; 2003US-047128BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Currie MG, Mahajan-Miklos S;
                                                                                                                                                                                                                                                                   28-JAN-2004; 2004WO-US002390
                                                                                                                                                                                                                                                                                                                  28-JAN-2003; 2003US-0443098P.
                                                                                                                                                                                                                                                                                                                                                                                                              (MICR-) MICROBIA INC.
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                                                                                                                       Escherichia coli
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Claim 3; Page 118; 133pp; English.
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100.0%; Pre
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(UYJE-) UNIV JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colorectal; metastasis.
                                             WPI; 1995-178646/23.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                       Sequence 18 AA;
                      Waldman SA;
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100.0%; Pred. No. 2.9e-13;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 19, Conservative
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New conjugated compounds are provided which consist of (1) an ST recepto binding molety and (2) an active moiety which is a radio- stable agent.
'ST refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapoutic agent methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugated cpds. which specifically bind to colorectal cancer cells -comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                   heat-stable toxin; conjugate; imaging; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                            AAR85956 standard; peptide; 18 AA
54 NNTFYCCELCCNPACAGCY 72
                                                                                                                                                                     ST Ia receptor ligand portion.
                                                                                                                                                                                                                                                                                                                                                                          93US-00141892.
94US-00305056.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                    colorectal; metastasis.
                                                                                                                                                                                                  ST; receptor; ligand;
                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                       19-JAN-1996
                                                                                                                                                                                                                                                                                                                                           26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1993;
                                                                                                                                                                                                                                                                               WO9511694-A1
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                                                                                                         AAR85956;
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Gaps

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0; Indels

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The invention relates to a conjugated compound that comprises a ST (heatstable toxin) receptor moiety selected from one of the sequences shown in AAY40508-Y40559 and an active moiety (antisense molecule). The compound is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells
                                                                                        The invention relates to a conjugated compound that comprises a ST (heatstable toxin) receptor moiety selected from one of the sequences shown in AAY40508-Y40559 and an active moiety (antisense molecule). The compound is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugated compound comprising a receptor moiety and active moiety, useful for the treatment/prevention of colorectal cancer.
compound comprising a receptor moiety and active moiety, the treatment/prevention of colorectal cancer.
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Pred. No. 1.2e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        94.7%; Score 18; DB 2; Length 18; 100.0%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY40518 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 25-26; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.7%; Scc...
100.0%; Pre
                                                          Claim 1; Col 35-36; 23pp; English.
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                                                                                                                                                                                                                                                                                                                18; Conservative
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
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    Conjugated
useful for
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ST refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleit acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       Conjugated cpds. which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                °;
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Pred. No. 1.2e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 117; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNTFYCCELCCNPACAGC 18
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94US-00305056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match .
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-571264/48
                                                                                                                                                                                                                                                                                                                    4PI; 1995-178646/23
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                              Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1993;
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                                                                  WO9511694-A1
                                                                                                                                               26-OCT-1994;
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                                                                                                                                                                                                                                                                                  Waldman SA;
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The specification describes a method for selecting a candidate drug compound having affinity for biological receptors. The method uses a combination of rational and combinatorial drug design techniques. At least I residue in the original cell receptor binding peptide is modified to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method is used for identification of a candidate receptor antagonist or agonist. The present peptide is a cell receptor binding peptide, and can thus be used as a starting point for identification of candidate drug compounds, used as a starting for identification of candidate drug compounds.
                                                                                                                                                                                                               Method of drug selection - and use of an acetamidomethyl-protected polymer as a substrate in the solid state synthesis of an oligopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macrocyclic complexing agents containing linked 2,6-pyridinylene nuclei as components of targeting immunoreagents binding to ST receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat stable ST enterotoxin; immunoreagent; radiological therapy; diagnosis; ST receptor binding moiety; macrocyclic complexing agent; tumour; infectious diarrhoeal disease; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wolfe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.7%; Score 18; DB 2; Le
100.0%; Pred. No. 1.2e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli heat stable ST enterotoxin STa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shah C, Black C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 39; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY29607 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                       Disclosure; Page 1; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NTFYCCELCCNPACAGCY 19
98WO-GB002504.
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                                      97GB-00017652
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                                                                          IMAGING AS
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Matches 18; Conservative
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                                                                                                                                                                         WPI; 1999-181156/15.
                                                                          (NYCO-) NYCOMED IM/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
20-AUG-1998;
                                      20-AUG-1997;
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                                                                                                                                  Wolfe HR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a conjugated compound that comprises a ST (heat-stable toxin) receptor moiety selected from one of the sequences shown in AAY40508-Y40559 and an active moiety (antisense molecule). The compound is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selection, candidate drug, cell receptor binding; affinity, biological receptor, rational drug design, combinatorial drug design, receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic; gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
                                                                                                                                                                                                           Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compound comprising a receptor molety and active molety, the treatment/prevention of colorectal cancer.
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                                                    AAY40512 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY02385 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
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                                                                                                                                                                     ST receptor binding peptide
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nes 18; Conserv
                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
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useful for
                                                                                        AAY40512;
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Matches

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Comprising a metal ion and a residue of a macrocylic complexing agent (MCA). Ti's are of use in diagnostic imaging and therapy of specific disease sites in a patient, using either radioactive, magnetic resonance, or fluorescent means of detection or use of the metal ion; alternatively, a substituent of these types may be introduced, e.g. radioactive iodine, co perform the same function. Most notable is the imaging and coline, correction therapy of tumours. In addition, a variety of bacteria, including Escherichia coli, vibrio cholerae, Citrobacter freundii, and corrected diseases, particularly in pediatrics and cause infectious diarrhoeal diseases, particularly in pediatrics and in developing countries. These types of diarrhoea can also be treated using TI's. TI's may specifically used to treat cancers and also be used as an antidiarrhoeal agent of trea free from the various disadvantages of prior art reagents, including rapid destruction and/or excretion, instability in storae, and protein degradation. There is no perturbation of protein reactive groups at the pyridyl chelating site. AAX29607 to camplification of the present invention
                            present invention describes targeting immunoreagents (TI's)
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Sequence 18 AA;

ö Gaps ö 94.7%; Score 18; DB 2; Length 18; 100.0%; Pred. No. 1.2e-12; ive 0; Mismatches 0; Indels Length 18; Local Similarity 100. ses 18; Conservative Query Match Matches

13 18 NTFYCCELCCNPACAGCY N

NTFYCCELCCNPACAGCY

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RESULT 12 AAY02397

AAY02397 standard; peptide; 18 AA AAY02397;

(first entry) 09-JUL-1999

Heat stable ST enterotoxin Sta.

Selection, candidate drug, cell receptor binding, affinity; biological receptor; rational drug design; combinatorial drug design; receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic; gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.

Escherichia coli,

WO9909417-A2

25-FEB-1999,

98WO-GB002510. 20-AUG-1998;

97GB-00017652. 20-AUG-1997;

NYCO-) NYCOMED IMAGING AS (COCK/) COCKBAIN J.

Wolfe HR;

WPI; 1999-181157/15

Method of drug selection - using a combination of rational and combinatorial drug design techniques.

Disclosure, Page 1, 35pp, English.

The specification describes a method for selecting a candidate drug compound having affinity for biological receptors. The method uses a combination of rational and combinatorial drug design techniques. At least 1 residue in the original cell receptor binding peptide is modified

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to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method is used for identification of a candidate receptor antagonist or agonist. The present peptide is a cell receptor binding peptide, and can thus be used as a starting point for identification of candidate drug compounds, using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anorectic, cardiovascular, candidatic, analgesic, CNS, respiratory, neuroprotective; vasotropic, auditory; antiemetic, antiathmatic; neuroprotective; vasotropic, auditory; antiemetic, antiathmatic; neuroprotective; vasotropic, virucide; immunosuppressive; antiallergic; antidabetic; ophthalmological; tranquiliser; hypnotic; nootropic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder; irritable bowel syndrome; constipation; gastroseophageal reflux disease; laritable bowel syndrome; constipation; gastroseophageal reflux disease; inflammatory bowel disease; obseity; heart failure; cystic fibrosis; cancer; respiratory disorder; neurological disorder; carbonate imbalance; erectile dysfunction; inner ear disorder; slow digestion; nausea; vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy; retinopathy; nephropathy; sleep disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified peptide (PI) capable of activating the guanylate cyclase C (GC-C) receptor. Further disclosed is a pharmaceutical composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastrointestinal disorder in a patient, which involves administering PI, where the gastrointestinal disorder is gastrointestinal motility disorder, irritable bowel syndrome, chronic constipation, a functional
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                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                               Score 18; DB 2; Length 18;
Pred. No. 1.2e-12;
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100.0%;
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15-MAY-2003; 2003US-0471288P.
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                                                                                                                                                                                                                                                                2 NTFYCCELCCNPACAGCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                       18; Conservative
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                                                                                                                                            Sequence 18 AA;
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cc gastrointestinal disorder, gastroesophageal reflux disease, functional heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia, cc gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-obstruction, chronic pseudo-obstruction, colonic pseudo-obstruction, cromario pseudo-cobstruction, cromario proposed disease. The peptide of the invention is also useful for treating cc desarty, congestive heart failure, cystic fibrosis or a patient suffering cromer, respiratory disorder, neurological disorder, disorder associated with carbonate imbalance, erectile dysfunction, insulin-related disorder or inner ear disorder. Pl is useful in treating slow digestion or slow stomach emptying. Pl is useful in realeving symptoms of gastroparesis continer ear disorder. Pl is useful in treating slow digestion or slow stomach emptying. Pl is useful in treating or preventing cuseful for treating or preventing cuseful for treating or preventing concluding inhalation. Pl is useful in treating or preventing retinopathy, nephropathy and edema formation. Pl is useful for treating or preventing concluding inhalation. Pl is useful in treating or preventing concluding inhalation. Pl is useful in treating or preventing concluding inhalation. Pl is useful in treating or preventing conformation. Pl is useful in treating integrate cells bearing GCC receptor, e.g., cystic therapeutic molecule to target cells bearing GCC receptor, e.g., cystic conformation in targeting radioactive moleties or therapeutic molecules to the conformation or the inteatinal treat, thus conformation or the intention of the grane of the grane of the gase. The properties of the grane of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colorectal/metastasised or local colorectal cancer. The current sequence represents a bacterial ST peptide which is an activator of the GC-C receptor. ST peptides are considered super agonists of GC-C and are very
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94.7%; Score 18; DB 8; Length 18; 100.0%; Pred. No. 1.2e-12; ive 0; Mismatches 0; Indels 1 NTFYCCELCCNPACAGCY 18 2 NTFYCCELCCNPACAGCY 19 Query Match Best Local Similarity 100.' Matches 18; Conservative ઠે

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Gaps ö

> ADR48332 standard; peptide; 18 AA. 04-NOV-2004 (first entry) C. freundiii ST peptide. ADR48332; RESULT 14 ADR48332

Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer; anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory; neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic; nephrotropic; bepatotropic; virucide; immunosuppressive; antiallergic; antidabetic; ophthalmological; tranquiliser; hypnotic; nootropic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder; irritable bowel syndrome; constibation; gastroseophageal reflux disease; heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis; inflammatory bowel disease; obesity; heart failure; cystic fibrosis; cancer; respiratory disorder; neurological disorder; carbonate imbalance; erectile dysfunction; inner ear disorder; slow digestion; nausea; vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy; retinopathy; nephropathy; headache; anxiety; sleep disorder.

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Citrobacter freundii
                           19-AUG-2004.
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28-JAN-2004; 2004WO-US002390

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The invention relates to a purified peptide (PI) capable of activating to the guanylate cyclase C (GC-C) receptor. Further disclosed is a pharmaceutical composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastrointestinal composition of the invention is useful for treating PI, where the disorder in a patient, which involves administering PI, where the gastrointestinal disorder intestinal disorder constitation, ronder and disorder constitation, ronder gastrointestinal disorder constitation, ronder gastrointestinal disorder. Consent gastrointestinal disorder constitation, rongestive heart failure, cystic fibrosis or a patient suffering cancer, respiratory disorder. Plis useful in relating symptoms of gastroparesis concert manager. Plis useful in relating symptoms of gastroparesis concert and saughant of preventing symptoms of gastroparesis concert in diabetes mallitue, bypesilycamia, respiratory disorder malerion. Plis useful for treating or preventing type II diabetes mallitue, hypesilycamia, respiratory disorder including inhalation. Plis useful in treating or preventing concert including inhalation. Plis useful for treating or preventing concert including inhalation. Plis useful stander conjugated to diagnosis disease, then an antient of the disorder and disease, tumours etc. Plis useful for treating or preventing confidence of the same lessons and specific cells hearing GC-C receptor, e.g., cystic consental measured beacher, each conjugated to diagnosis of the conjug
                                                                                                                                                                                                                                                Novel purified peptide capable of activating the guanylate cyclase C receptor, useful for treating obesity, congestive heart failure and benign prostatic hyperplasia.
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28-JAN-2003; 2003US-0443098P.
15-MAY-2003; 2003US-0471288P.
12-NOV-2003; 2003US-0519460P.
                                                                                                                                                     Currie MG, Mahajan-Miklos S;
                                                                                                  (MICR-) MICROBIA INC.
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Gaps ö Length 18; 0; Indels 1.2e-12; Score 18; DB 8; Mismatches 94.7%; Scc... 100.0%; Pre Query Match
Best Local Similarity 100.
Matches 18; Conservative

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2 NTFYCCELCCNPACAGCY 19 1 NTFYCCELCCNPACAGCY 18 ð 셤

RESULT 15 ADR48341

ADR48341 standard, peptide, 18 AA. 04-NOV-2004 (first entry) Bacterial ST peptide #2. ADR48341; XXXXXX

anorectic, cardiovascular, constants, candional anorectic, cardiovascular, cytostatic, analgesic, CNS; respiratory, neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic; nephrotropic; virucie; immunosuppressive; antiallergic; antidiabettc; ophthalmological; tranquiliser; hypnotic; nootropic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder; haritable bowel syndrome; constipation; gastroophageal reflux disease; inflammatory bowel disease; obesity; heart failure; cystic fibrosis; encert; respiracy disorder; neurological disorder; carbonate imbalance; erectile dysfunction; inner ear disorder; slow digestion; nausea; vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy; cardiant; antiulcer; retinopathy; nephropathy; headache; anxiety; sleep disorder. Gastrointestinal; antiinflammatory;

Sacherichia coli

WO2004069165-A2

19-AUG-2004.

28-JAN-2004; 2004WO-US002390

28-JAN-2003; 2003US-0443098P. 15-MAY-2003; 2003US-0471288P. 12-NOV-2003; 2003US-0519460P.

(MICR-) MICROBIA INC.

Currie MG, Mahajan-Miklos S;

WPI; 2004-604332/58.

Novel purified peptide capable of activating the guanylate cyclase C receptor, useful for treating obesity, congestive heart failure and benign prostatic hyperplasia.

Disclosure; Page 29; 93pp; English.

The invention relates to a purified peptide (P1) capable of activating the guanylate cyclase C (GC-C) receptor. Further disclosed is a pharmaccutical composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastroincestinal disorder is a patient, which involves administering P1, where the captorinestinal disorder is gastrointestinal motifility disorder. In the invention is useful for treating P1, where the castroincestinal disorder is gastrointestinal motifility disorder. In the invention is a functional castroincestinal disorder, gastroopshages in feltura disease, functional dyspepsia, nonlicer dyspepsia, functional dyspepsia, nonlicer dyspepsia, constitution, clonic pseudocobstruction, crompstruction, crompstruction adisease. The peptide of the invention is also useful for treating disease. The peptide of the invention is also useful for treating for constitution, the P1/GC-C receptor agonist is useful for treating crompstruction. The P1/GC-C receptor agonist is useful for treating crompstruction. The P1/GC-C receptor agonist is useful for treating crompstruction. The P1/GC-C receptor agonist is useful for treating crompstruction, insulin-related disorder with castronate imbalance, erectile dysfunction, insulin-related disorder crompstruction, respiratory disorder. Pi su useful in relating symptome of gastric emptying. Pl is useful in treating or preventing cueful for treating or preventing crompstruction, insuling inhalation. Pl is useful for treating or preventing crompstruction and consist is an endomed conficient of the small intestine, including crompstruction conficient of the small intestine, including crompstruction conficient of the small intestine, including crompstruction conficient molecule to target cells bearing GC- croeptor, erg. cyptic cibrosis lesions and specific cells lining the intesting crompstructure collected, many and dispense or language of the small intestine, including cells lining or treating crompstruction colorcetal/metassised

receptor. ST peptides are considered super agonists of GC-C and are very resistant to proteolytic degradation. ខ្លង្គមូន

Sequence 18 AA;

Gaps ö Length 18; 0; Indels 94.7%; Score 18; DB 8; Le 100.0%; Pred. No. 1.2e-12; 100.0%; Prec. ...

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                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Word size :
                                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                              Run on:
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No.
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APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
TORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STRYES: Pennsylvania
COUNTRY: U.S.A.
ZIP: 1910
XIP: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATER: PC-DOS/MS-DOS
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Pred. No. 8.9e-14;
; Mismatches 0;
US-08-583-447A-19

US-08-583-447A-11

US-08-467-920-8

US-08-467-920-41

US-08-467-920-41

US-08-635-930-8

US-08-635-930-8

US-08-635-930-14

US-08-635-930-14

US-08-193-997-14

US-09-193-997-14

US-09-193-997-14

US-09-138-237A-14

US-09-138-237A-14

US-09-138-237A-14

US-09-138-237A-14

US-09-138-237A-14

US-09-138-237A-14

US-09-138-237A-14

US-09-148-92A-15

US-08-141-892A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-00T-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECHONE: 215-568-3100
TELEPAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-550 CO. 2: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
    TOPOLOGY: linear
MOLECULE TYPE: protein
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GENREAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions That Specifically Bind To TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using TITLE OF INVENTION: The Same
TITLE OF INVENTION: The Same
TITLE OF INVENTION: The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WordPerfect 6.0/6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,930
FILING DATE: 26-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: WAS THE TABLE TABLES THE TABLES THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Worderfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/141,892
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/141,892
FILING DATE: Z6-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
REFERENCE/DOCKET NUMBER: TJU-1589
TELECHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08635930 Patent No. 6060037
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-467-920-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                           RESULT 2
US-08-583-447A-2
is Sequence 2. Application US/08583447A
is Sequence 2. Application US/08583447A
is Patent No. 5879556
is GENERAL INFORMATION:
is APPLICANT: Waldman, Scott A.
it TILE OF INVENTION: Receptor Binding Compounds and TITLE OF INVENTION: ST Receptor Binding the Same NUMBER OF SEQUENCES: 56
is CORRESPONDENCE ADDRESS: 56
is CORRESPONDENCE ADDRESS: 56
is STREET: One Liberty Place, 46th Floor CITY: Philadelphia
is STATE: Pennsylvania
is COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 2; Length 19; 100.0%; Pred. No. 8.9e-14; tive 0; Mismatches 0; Indels
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| Sequence 2, Application US/08467920
| Sequence 2, Application US/08467920
| Sequence 2, Application US/08467920
| Sequence 2, Application Secure 3, Sequence 2, Application:
| APPLICAMT: Waldman, Scott A. TITLE OF INVENTION: End Of Colorectal Cancer Cells TITLE OF INVENTION: Bind To Colorectal Cancer Cells TITLE OF INVENTION: And Methods Of Using The Same NUMBER OF SEQUENCES: 54
| CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5962220ris |
| STREET: One Liberty Place, 46th Floor |
| STREET: Pennsylvania |
| STATE: Pennsylvania |
| COUNTRY: USA |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWATING SYSTEM: WILLOWER
SOFTWARE: WORDERECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA: MARK
REGISTRATION NUMBER: 33,229
REFERENCE/POCKET NUMBER: TUU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-56-3100
TELEPHONE: 215-360-3100
TELEPHONE: 215-560-3100
TELEPHONE: 215-560-3100
TELEPHONE: 215-560-3100
TELEPHONE: 215-560-3100
TELEPHONE: 215-560-3100
TELEPHONE: 215-360-3100
TELEPHONE: 215-360-3100
TELEPHONE: 215-360-3100
TELEPHONE: 215-360-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NNTFYCCELCCNPACAGCY 19
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
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Gaps
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Length 19;
           Indels
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NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REPRENCE/DOCKET NUMBER: TUU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08141892A; Patent No. 5518888
GENERAL INFORMATION:
                                                           i NNTFYCCELCCNPACAGCY 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-138-237A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 8.9e-14; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 3; Length 19; 100.0%; Pred. No. 8.9e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09193997

Patent No. 6087109

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions That Specifically
Bind To Colorectal Cancer Cells
And Methods Of Using The Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DAYE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REPREMECE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3139
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                               TJU-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/193,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 33,22.
REFRENCE/DOCKET NUMBER: TJU-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
; INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         1 NNTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                1 NNTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NNTFYCCELCCNPACAGCY 19
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-635-930-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-09-193-997-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
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US-09-193-997-2
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JOSTICS APPLICATION US/09138237A

Sequence 2, Application US/09138237A

Patent No. 6268159

GENERAL INFORMATION:
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
TUTLE OF INVENTION:
CORRESPONDENCE: 54

CORRESPONDENCE: Mondowck Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Waldman, Scott A.

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods

TITLE OF INVENTION: OF Using the Same

TITLE OF INVENTION: OF Using the Same

TITLE OF INVENTION: OF Using the Same

TORRESPONDENCE: 54

CORRESPONDENCE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris

STREFT: One Liberty Place - 46th Floor

CITY: 'Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 3; Length 19; 100.0%; Pred. No. 8.9e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103
COMPUTER READABLE FORM:
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Gaps

; 0

Score 18; DB 1; Length 18; Pred. No. 9.6e-13;

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94.7%; Scor.
100.0%; Pred. No. 9...
                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.(
Matches 18; Conservative
                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-141-892A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-38
                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           US-08-141-892A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08141892A

Patent No. 551888

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: of Using the Same
ITILE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 1; Length 18;
Pred. No. 9.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; Scor.
100.0%; Pred. No.
MEDIUM TYPE: 3.5 inch disk, 720 Kb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/141,892A PRIOR APPLICATION NUMBER: APPLICATION NUMBER: ATTONNEY/AGENT INFORMATION: NAME: Debuce, Mark REGISTRATION NUMBER: 33,229 REFERENCE/DOCKET NUMBER: TJU-0903 TELECHONE: 215-568-3100
TELECHONE: 215-568-3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NNTFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNTFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
....hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-141-892A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-141-892A-7
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Sequence 38, Application US/08141892A

Patent No. 551888

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION:

TITLE OF INVENTION: of Using the Same

TITLE OF INVENTION: of Using the Same

TITLE OF INVENTION: of Using the Same

NUMBER OF SEQUENCES:

ADDRESSE: woodcock Washburn Kurtz Mackiewicz and No. 5518888ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: OPERATINE: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.7%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 9.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scott A.
ST Receptor Binding Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08583447A Patent No. 5879656 GENERAL INFORMATION: Scott A. TITLE OF INVENTION: ST Receptor B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-OCT-1993
CLASSIFICATION 435
PRIOR APPLICATION 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0
TELEPONE: 215-56-310
TELEPONE: 215-56-310
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NTFYCCELCCNPACAGCY 18
2 NTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NTFYCCELCCNPACAGCY 19
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No.
                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 18; DB 2; Lv
100.0%; Pred. No. 9.6e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordberfeet 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION WHERE: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                       NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NTFYCCELCCNPACAGCY 19
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103
                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                        US-08-583-447A-13
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USCO06-583-447A-13

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USCO06-583-447A-13

USCO06-583-447A-13

USCO06-583-447A-13

USCO06-583-447A-10N

ITTLE OF INVENTION: ST Receptor Binding Compounds and TITLE OF INVENTION: Methods of Using the Same

UNUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris STRET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA
                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
  Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Wordberfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTONNEY, AGENT INFORMATION:
NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 31,229
REGISTRATION NUMBER: 31,229
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%; Score 18;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NNTFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                              ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-583-447A-7
TITLE OF INVENTION: Mel
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
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STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPETECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SOLES.
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
ATTORNEY/ABRNT INFORMATION:
NAME: DeLuca Mark
REGISTRATION NUMBER: 33,229
REPERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELECAMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 13:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rrpE: amino acid;
; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
                                                                            Pennsylvania
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19103
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-467-920-38
                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                 Sequence 77, Application US/08467920

Patent No. 596220

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5962220Tis
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13. Application US/08467920
Sequence 13. Application US/08467920
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR PAPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                           NTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NNTFYCCELCCNPACAGC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-920-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-467-920-13
                                                                                                                                                      RESULT 13
US-08-467-920-7
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Length 18;
                                                                                                                                                                                                                                                                                              Sequence 38. Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
   APPLICANT: Waldman, Scott A.
   TITLE OF INVENTION: And Methods Of Using The Same
   TITLE OF INVENTION: And Methods Of Using The Same
   NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
   ADDRESSEE: Wo. 5962220ris
   STREET: One Liberty Place, 46th Floor
   CITY: Philadelphia
   STATE: Pennsylvania
Query Match

94.7%; Score 18; DB 2; L
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0;
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; 0

Search completed: March 26, 2005, 17:27:26 Job time: 25.7857 secs

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Sequence Sequence Sequence Sequence Sequence

US-10-621-684-16
US-10-621-684-42
US-10-621-684-11
US-10-621-684-13
US-10-621-684-13
US-10-621-684-43
US-10-621-684-45
US-10-621-684-35
US-10-796-719-25
US-10-796-719-39
US-10-796-719-30

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Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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                                                                                                                                                                                   March 26, 2005, 17:25:02 ; Search time 61.4107 Seconds (without alignments) 102.440 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, 7 Sequence 7, M. Sequence 13, 4 Sequence 2, M. Sequence 4, M. Sequence 14, M. Sequence 11, M. Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-621-684-13
US-10-621-684-13
US-10-621-684-13
US-10-621-684-13
US-10-621-684-13
US-10-621-684-14
US-10-621-684-14
US-10-621-684-14
US-10-621-684-15
US-10-621-684-15
US-10-621-684-15
US-10-621-684-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1407402 segs, 331100923 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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                                                                                                                                      - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0
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94.7
94.7
94.7
94.7
99.5
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                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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                                                                                                                                   OM protein
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                Run on:
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RESULT 1

US-10-621-684-2

Sequence 2, Application US/10621684

Publication No. US20040029182A1

Sequence 2, Application US/10621684

Publication No. US20040029182A1

GENERAL INFORMATION:

Methods of Using the Same
Methods of Using the Same
Methods of Using the Same
NUMBER OF EXQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

STREET: On Liberty Place, 46th Floor

CITY: Philadelphia
STREET: One Liberty Place, 46th Floor

COMPUTER: Philadelphia
STREET: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

COMPUTER: Philadelphia
STREET: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

COMPUTER: Philadelphia
STREET: Woodcock 46th Floor

COMPUTER: Wordberfect 6.1

CURRENT APPLICATION NUMBER: US/10/621,684

FILING DATE: 11-011-003

CURRENT APPLICATION NUMBER: US/10/621,684

FILING DATE: 05-0444.1996

PRILAMO BATE: 66-067-1993

ATTORNEY ABERT INFORMATION:

NAME: BEGISTRATION NUMBER: US/08/141,892

FILING DATE: 66-067-1993

ATTORNEY ABERNEY NUMBER: 13.229

REFERENCE/DOCKET NUMBER: 13.29

REFERENCE/DOCKET NUMBER: 13.00

TELECOMMUTCATION NUMBER: 13.00

TELECOMMUTCATION NUMBER: 13.00
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COUNTRY: USA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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APPLICANT: Curia, Mark G.

APPLICANT: Curia, Mark G.

APPLICANT: Mahajan-Mklos, Shalina
APPLICANT: Mahajan-Mklos, Shalina
TITLE OF INVENTION: METADDS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS;
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US/10/796,719
FRIOR FILING DATE: 2004-03-09
PRIOR FILING DATE: 2004-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2003-01-16
SPIOR FILING DATE: 2003-01-11-12
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                100.0%; Score 19; DB 15; Length 19; 100.0%; Pred. No. 6.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-10-21-08-7,
S-10-21-08-7,
S-Quence 7, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 19; DB 17;

Best Local Similarity 100.0%; Pred. No. 1.6e-13;

Matches 19; Conservative 0; Mismatches 0;
                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-796-719-20
Sequence 20, Application US/10796719
Publication No. US20050020811A1
GENERAL INFORMATION:
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                       1 NNTFYCCELCCNPACAGCY 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 NNTFYCCELCCNPACAGCY 72
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Escherichia coli
US-10-796-719-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                       US-10-621-684-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-10-621-684-7
                                                                                                                                                                                                                                                                                                                                                                             a
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Mithods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 94.7%; Score 18; DB 15; L. Best Local Similarity 100.0%; Pred. No. 7.2e-13; Matches 18; Conservative 0; Mismatches 0;
                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-301-2003
CLASSIFICATION 1435
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-13N-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-10AN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DeLuca, Mark
REGISTRATION NUMBER: 33, 229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-621-684-7
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10621684
Publication No. US20040029182A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NNTFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103
COMPUTER READABLE FORM:
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                                                                                                                          SUBJECTATION INTERCENTATION.

JUNEARY INTERCENT: Mahajan-Miklos, Shalina
APPLICANT: Mahajan-Miklos, Shalina
JITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US/10/796,719
CURRENT PILING DATE: 2004-01-29
PRIOR FILING DATE: 2004-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR PILING DATE: 2003-01-28
PRIOR PILING DATE: 2003-01-28
PRIOR PELING DATE: 2003-01-28
PRIOR PELING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/471,288
PRIOR PELING DATE: 2003-01-12
PRIOR FILING DATE: 2003-01-12
PRIOR FILING DATE: 2003-11-12
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FASTESED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 17; I
Pred. No. 7.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                              Sequence 2, Application US/10796719
Publication No. US20050020811A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Scallarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NTFYCCELCCNPACAGCY 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Citrobacter freundii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conservat
                                                             JS-10-796-719-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-796-719-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                        DB 15; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 15; I Fred. No. 7.2e-13; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-UN1-2003
CLASSIFICATION: 435
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHRRACTERISTICS:
LENGTH: 18 amino acida
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                      94.7%; Score 18; DB
100.0%; Pred. No. 7.2
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMUNICATION INFORMATION.
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CIARRACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                    1 NTFYCCELCCNPACAGCY 18
                                                                                                                                                                                                                                                                                 2 NTFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.7%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.79
Best Local Similarity 100.9
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19103
                                                                                                                                                                    US-10-621-684-13
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-10-61-684-41

Sequence 41, Application US/10621684

Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION:

Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.5%; Score 17; DB 15; L
100.0%; Pred. No. 8.4e-12;
tive 0; Mismatches 0;
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Worldows
SOFTWARE: Worldows
SOFTWARE: Worldows
SOFTWARE: Worldows
SOFTWARE: Worldows
SOFTWARE: Worldows
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-011-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
PILING DATE: 05-0AN-1996
APPLICATION NUMBER: US/08/141,892
FILING DATE: 05-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-310
TELEPHONE: 215-568-3100
TELEPHONE: 11-000: 14:
SEQUENCE CHARACTERISTICS:
TENNORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORPUTER: WATCHERIECT
COMPUTER: WATCHERIECT
COMP
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TOPOLOGY: linear
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MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-621-684-14
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NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TFYCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TFYCCELCCNPACAGCY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 17; Conservative
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
CUUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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US-10-621-684-14
i Sequence 14, Application US/10621684
i Publication No. US20040029182A1
i GENERAL INFORMATION:
i APPLICANT: Waldman, Scott A.
TITLE OF INVENTION:
Methods of Using the Same
                                                                                                                                                       Sequence 8, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%; Score 17; DB 15; Length 17; ilarity 100.0%; Pred. No. 8.4e-12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DAYS.

APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGNT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEPRAK: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Intear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-621-684-8
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1 NTFYCCELCCNPACAGCY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTFYCCELCCNPACAGC 17
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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tes 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103
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                                                                                                                              US-10-621-684-8
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Best Local S
Matches 17
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Length 17; Indels

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILLING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 0S-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                        Sequence 15, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.2%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FYCCELCCNPACAGCY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi.
Matches 16;
                                                                                                       US-10-621-684-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 16; DB 15; Length 16; 100.0%; Pred. No. 9.9e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                89.5%; Score 17; DB 15; I
ilarity 100.0%; Pred. No. 8.4e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/583,447A
FILING DATE: 26-OCT-1993
FILING DATE: 26-OCT-1993
    TJU-1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFREBUCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 41: US-10-621-684-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-621-684-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                          TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 215-568-3100
                                                                                                                          LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                           TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   2 NTFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                         1 NTFYCCELCCNPACAGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TFYCCELCCNPACAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                 Local Similarity
hes 17; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-621-684-9
                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 17
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-10-621-684-42
i Sequence 42, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION:

Methods of Using the Same
                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                        Query Match
78.9%; Score 15; DB 15; I
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.9%; Score 15; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-09; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM PC COMPATIBLE
COMPUTER: TEMP PC COMPATIBLE
SOFTWARE: WATGBEFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 42: US-10-621-684-42
REFERENCE/DOCKET NUMBER: TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPK: 215-568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 42
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                            5 YCCELCCNPACAGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YCCELCCNPACAGCY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                 US-10-621-684-16
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CORRESSONDEMESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
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VS-10-621-684-16
VS-10-621-684-16
Sequence 16, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION:
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.9%; Score 15; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-09; Matches 15; Conservative 0; Mismatches 0;
                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTHARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-JU1-2003
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/583,447A
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US/08/141,892
FILING DATE: 26-CCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPITER: 1BM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-011-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/583,447A FILING DATE: 05-JAN-1996 APPLICATION NUMBER: US 08/141,892 FILING DATE: 26-OCT-1993 ATTORNEY/AGENT INFORMATION: NAME: DELUCA, Mark
                                                                                                                                                                                                                                                                                                                                                                                 NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FYCCELCCNPACAGC 15
       ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-621-684-10
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Won Mar 28 09:44:13 2005

S YCCELCCNPACAGCY 19 ||||||||||||||||||1 1 YCCELCCNPACAGCY 15

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Search completed: March 26, 2005, 17:44:30 Job time: 61.4107 secs

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version 5.1.6
- 2005 Compugen Ltd.
 GenCore
Copyright (c) 1993
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protein search, using sw model OM protein

Run on:

March 26, 2005, 17:10:31 ; Search time 19.6786 Seconds (without alignments) 92.899 Million cell updates/sec

1 NNTFYCCELCCNPACAGCY 19 US-10-775-481A-2 Perfect score: Sequence: Title:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 seqs, 96216763 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	19	100.0		<u> </u>	QHEC1	heat-stable entero
7	18	94.7		Ņ	A60103	heat-stable entero
Э	11	57.9	72	Н	QHEC4	heat-stable entero
4	11	57.9	72	-	QHECIB	heat-stable entero
ß	10	52.6	18	-	QHEC2	heat-stable entero
9	10	52.6	53	~	\$68705	heat-stable entero
7	6	47.4	99	~	S31652	enterotoxin - Yers
89	6	47.4	71	N	S25659	heat-stable entero
60	9	31.6	13	~	A28953	alpha-conotoxin SI
10	9	31.6	15	н	NTKNAG	alpha-conotoxin GI
11	9	31.6	17	~	A54534	heat-stable entero
12	9		19	7	A44379	alpha-conotoxin SI
13	9	31.6	65	7	S34671	heat-stable entero
14	9		78	H	QHVC1	heat-stable entero
15	φ	31.6	90	~	D85845	probable lysis pro
16	9		620	7	H82761	sulfur deprivation
17	9	31.6	924	~	E71476	alanine-tRNA ligas
18	S	26.3	55	ď	S14212	NADH2 dehydrogenas
19	ស	26.3	75	N	H84631	hypothetical prote
20	ß	26.3	108	~	AF1043	hypothetical prote
21	ស	26.3	110	~	174319	н
22	ស	ဖ	111	~	B72476	hypothetical prote
23	ß	9	116	~	S75378	hypothetical prote
24	S	26.3	124	N	C96762	hypothetical prote
25	ß	26.3	129	N	A24255	lass
56	S	9	132	0	AI0543	probable secreted
27	ហ	φ		~	T17300	hypothetical prote
28	ហ	26.3		0	S34815	nifUl protein - Rh
53	Ŋ	26.3	7	Н	Q2BP87	gene 2.8 protein -

-ને	hypothetical prote	probable rRNA meth	BioY family protei	conserved hypothet	probable pentose-5	hypothetical prote	aquaporin homolog	protein ZC123.3 [i	cob(I)alamin adeno					
H69051	G90169 F84494	E71464	A81681	F81726	D95865	T20398	T21359	F70405	D85888	A91044	873385	T12999	G87721	AG0814
0	2 0	~	~	0	~	~	~	0	7	~	7	7	7	~
145	146	187	196	224	228	230	232	235	243	243	254	256	263	265
26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3
ro r	տ տ	'n	Ŋ	S	Ŋ	Ŋ	ស	Ŋ	Ŋ	ഗ	Ŋ	ß	Ŋ	Ŋ
30	31	33.	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

				09-Jul-20				encoding		
				change				Tn1681		
RESULT 1	heat-stable enterotoxin ST-I precursor - Escherichia coli	N;Alternate names: heat-stable enterotoxin estAl	C;Species: Escherichia coli	C;Date: 31-Aug-1980 #sequence revision 31-Aug-1980 #text	C; Accession: A01822; A30985; A36732; JT0374; I51932	R; So, M.; McCarthy, B.J.	Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980	A; Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding	A; Reference number: A01822; MUID: 81054703; PMID: 6254008	

a heat-stale (S

004

A,Accession: A01822 Molecule type: DNA A,Residues: 1-72 <Laz> A,Cross-references: UNIPROT: P01559, GB: V00612, GB: J01831; NID: 943704; PIDN: CAA23883.1; P R,Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S. Can. J. Biochem. Cell Biol. 61, 287-292, 1983 A,Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of A,Reference number: A30985; MUID: 83284515; PMID: 6349752

A; Molecule type: protein A; Residues: 55-72 < LAZ2> A;Accession: A30985

A, Experimental source: strain Fl1

J. Bacteriol. 172, 5490-5493, 1990
A. Title: The heat-stable toxin I gene from Escherichia coli 18D. A. Reference number. A36732; MUID:90368614; PMID:2203756 A;Accession: A36732

A; Molecule type: DNA A; Residues: 1-72 <DAL> A; Residues: 1-72 <DAL> A; Cross-references: GB:MS8746; NID:g145860; PIDN:AAA62776.1; PID:g145861 A; Experimental source: strain 18D A; Experimental source: strain 18D R; Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;

RiStieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubiss, L.; Bolivar, F.; Blasmid 20, 42-53, 1988
A.fitle: Cloning, sequencing, and expression in ficoll-generated minicells of an Eschern A.Reference number: JT0373; MUID:89202548; PMID:3071819

A; Accession: JT0374

A;Molecule type: DNA A;Residues: 1.72 <STIX-R;Sekizaki, T.; Akashi, H.; Terakado, N. R;Sekizaki, T.; Akashi, H.; Terakado, N. Am. J. Vet. Res. 46, 909-912, 1985 A;Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin A;Reference number: IS1932; MUID:85249571; PMID:2990268 A; Accession: I51932

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Mosidues: 1-69.'P',71-72 <RES. A;Gross-references: GB:M25607; NID:g147877; PIDN:AAA24653.1; PID:g147878 C;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra

C, Superfamily: heat-stable enterotoxin ST C, Keywords: enterotoxin; heat-stable protein

```
Meat-stable enterotoxin ST-Ib precursor - Escherichia coli
NiAlternate names: heat-stable enterotoxin ST-A2
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: JS0292; A33069; A33067; A30567
R;Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A;Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A;Reference number: JS0292; MUID:83184648; PMID:6341230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:047185; UNIPROT:P07965; GB:M34916; NID:g146407; PIDN:AAA23996 R;Dwarakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, P Gene B1, 219-226, 1989
A;Fitle: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escheric A;Reference number: A33068; MUID:90034194; PMID:2680769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-18, A', 20-72 < DWA>
A; Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A; Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A; Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
A; Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
R; Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
Bur. J. Biochem. 129, 257-263, 1982
Bur. J. Bur. J. Biochem. 129, 257-263, 1982
A; Fitle: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic
A; Reference number: A33067; MUID:83105138; PMID:6759126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Molecule type: protein
;Residues: 54-72 <AIM>
;Guzman-Verduzco, L.M.; Kupersztoch, Y.M.
fodt. Immun. 57, 645-648, 1989
nfect. Immun. 57, 645-648, 1989
;Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chan, S.K.; Gdannella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A;Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat?
A;Reference number: A01823; MUID:81264141; PMID:7021541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
;Residues: 1-18, A', 20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
;Residues: 1-18, A', 20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
;Residues: 118, A', A', 20-24,'AG', 20-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
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C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
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Superfamily: heat-stable protein;

Seywords: enterotoxin; heat-stable protein

1-33/comain: signal sequence and propeptide #status predicted <SIG>

1-34-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>

1-39-64,60-68,63-71/Disulfide bonds: #status experimental
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   5 YCCELCCNPAC 15
                                                                         58 YCCELCCNPAC 68
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A; Residues: 1-72 < MOS>
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Heat-stable enterotoxin STA4 precursor - Escherichia coli
C,Species: Escherichia coli
C,Species: Bacherichia coli
C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
R,Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
A,Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiGuarino, A.; Giannella, R.; Thompson, M.R.
Thfect. Immun. 57, 649-652, 1998
A;Title: Citrobacter freundijpsp
A;Reference number: A60103; MUID:89108617; PMID:2912902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P07965; GB:J03311; NID:g147875; PIDN:AAA24652.1; PID:g147876
R;Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
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A;Reference number: A35978; MUID:90273381; PMID:2190361
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heat-stable enterotoxin ST-Ia - Citrobacter freundii
C;Species: Citrobacter freundii
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60103
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                                                                             experimental <MAT>
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;1-19/Domain: signal sequence #status predicted <SIG>
;20-53/Domain: propeptide #status predicted <PRO>
;54-72/Product: heat-stable enterotoxin #status predicted <MAT>
;59-64,60-68,63-71/Disulfide bonds: #status predicted
                                                                                                                                                                                     100.0%; Score 19; DB 1; Length 72 100.0%; Pred. No. 2e-15;
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-84/Domain: propeptide #status predicted <PRO>
F;55-72/Product: heat-stable enterotoxin ST-I #status
F;55-64,60-68,63-71/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                   0; Mismatches
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C;Superfamily: heat-stable enterotoxin ST
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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A; Residues: 1-18 < GUA>
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A; Residues: 1-72 <STI>
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A;Residues: 1-72 <ZHO>
C;Genetics:
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S25659; A41474; A33114; S65849
C;Accession: S25659; A41474; A33114; S65849
R;Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
FEMS Microbiol. Lett. 97, 63-66, 1992
A;Title: The polymerase chain reaction: an epidemiological tool to differentiate between A;Reference number: S25659
A;Accession: S25659
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Infect. Inmun. 58, 2983-2988, 1990
A;Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-A;Reference number: A41474; MUID:90354067; PMID:2201642
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A;Molecule type: DNA
A;Residues: 1-47,'S', 49-71 <DEL>
A;Residues: 1-47,'S', 49-71 <DEL>
A;Cross-references: GB:U09235; NID:g487394; PIDN:AAA18472.1; PID:g487395
B;TaXao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.
Bur. J. Biochem. 152, 199-206, 1985
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C;Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin
C;Superfamily: alpha-conotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced A;Reference number: A23114; MUID:86004705; PMID:4043080
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A;Residues: 54-71 <TAK>
R;Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Delorobiol. 14, 905-915, 1994
A;Title: Regulation of the Yersinia enterocolitica enterotoxin Yst gene. Influence of A;Reference number: S65849; MUID:95231297; PMID:7715452
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A;Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI. A;Reference number: A28953; MUID:89062448; PMID:3196703
                                                                               C;Species: Yersinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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C;Species: Conus striatus (striated cone)
C;Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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                                                 heat-stable enterotoxin yst precursor - Yersinia enterocolitica
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-41/Domain: propeptide #status predicted <PRO>
F;42-71/Product: heat-stable enterotoxin yst #status predicted
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40.0%; Pred. No. 0.00095;
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A;Cross-references: EMBL:U09235
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Matches 9; Conserv
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A,Residues: 1-71 <IBR>
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A;Molecule type: protein
A;Residues: 1-18 <CHA>
A;Residues: 1-18 <CHA>
A;Residues: 1-18 <CHA>
A;Rossidues: UNIPROT:P01560
A;Experimental source: strain 18D, serotype 0.42:k86:H37
C;Comment: This enterotoxin is one of several, of differing molecular sizes, produced by idues of the heat-stable enterotoxin ST-I
C;Royerfamily: heat-stable enterotoxin ST-C;Royerfamily: heat-stable protein
C;Roymords: enterotoxin; heat-stable enterotoxin ST-2 #status experimental <MAT>
F;1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
S68705
heat-stable enterotoxin Y-STc - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 25-Reb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Date: 25-Reb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: 568705
A;Yothino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FEBS Lett. 362, 319-322, 1995
A;Atitle: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A;Accession: 568705
A;Accession: 568705
A;Accession: 568705
A;Molecule type: protein
A;Residues: 1-53 405>
A;Molecule type: protein
A;Residues: 1-53 405>
A;Molecule type: protein
A;Residues: atrain 86-11
C;Superfamily: heat-stable enterotoxin; heat-stable protein
F;41-46,42-50,45-53/Disulfide bonds: #status predicted
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A;Molecule type: DNA
A;Residues: 1-66 < IBR>
A;Cross-references: UNIPROT:P31518; EMBL:X69218; NID:948617; PIDN:CAA49152.1; PID:948618
C;Superfamily: heat-stable enterotoxin ST
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$31652
enterotoxin - Yersinia kristensenii
C;Species: Yersinia kristensenii
C;Species: Yersinia kristensenii
C;Decession: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31652
R;Ibrahim, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Pred. No. 2.5e-05;
iive 0; Mismatches 0;
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A;Accession: S31652
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Best Local Similarity
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Matches

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Best Loca Matches

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FEMS Microbiol. Lett. 79, 105-110, 1991
Affile: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicus
A;Reference number: A54534
A;Accession: A54534
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A;Molecule type: protein
A;Residues: 1-19 «RAM»
A;Cross-references: CAS:143294-31-9; PIDN:AAB23762.1; PID:g257934
A;Experimental source: venom
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by chemical sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by chemical community. This peptide is an acetylcholine receptor blocker.
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C;Daces: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34671
R;Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.
submitted to the EmBL Data Library, July 1993
A;Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymeras
A;Reference number: S34671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A44379
E;Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R.
Biochemistry 31, 9919-9926, 1992
A;Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A;Reference number: A44379; MUID:93003172; PMID:1390774
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C;Reywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom
F;2-18,3-8,4-14/Disulfide bonds: #status predicted
F;19/Modified site: amidated carboxyl end (Ser) #status absent
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                         Query Match 31.6%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%; Score 6; DB 2;
100.0%; Pred. No. 2.9;
tive 0; Mismatches
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100.0%; Pred. No. 1.2;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lpha-conotoxin SII - cone shell (Conus striatus);Species: Conus striatus (striated cone)
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C;Superfamily: heat-stable enterotoxin ST
                                                                                                                                    A;Status: preliminary
Molecule type: protein
A;Residues: 1-17 <ARI-
C;Superfamily: heat-stable enterotoxin ST
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Best Local Similarity 100.
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-65 <ROS>
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Best Local S
Matches 6
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J. Biol. Chem. 258, 12247-12251, 1983
J. Biol. Chem. 258, 12247-12251, 1983
A; Title: Conotoxin MT. Disulfide bonding and conformational states.
A; Title: Conotoxin MT. Disulfide bonding and conformational states.
A; Contents: annotation; disulfide bonds
R; Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.
R; Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.
A; Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13
R; Guddat, L.W.; Martin, J.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.
B; Gootemistry 35, 11329-11335, 1996
A; Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resoluting A; Reference number: ASBS22, WMID:96738624; PMID:8784187
A; Contents: annotation; X-ray crystallography, 1.2 angstroms
R; Pardi, A.; Galdes, A.; Florance, J.; Maniconte, D.
Biochemistry 28, 5494-5501, 1989
A; Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NAR spendiculation structures of alpha-conotoxin GI determined by two-dimensional NAR spendiculation structures of alpha-conotoxin GI determined by two-dimensional NAR spendiculation structures of alpha-conotoxin GI determined by two-dimensional NAR spendiculation structures of alpha-conotoxin GI determined by two-dimensional NAR spendiculation structures of alpha-conotoxin GI determined by two-dimensional NAR A; Contents: annotation; Conformation by (1)H-NNR
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C; Superfamily: alpha-conotoxin
C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl en
F;1-15/Product: conotoxin GIA #status experimental <GIA>
F;1-13/Product: conotoxin GI #status experimental <GIC>
F;2-7,3-13/Disulfide bonds: #link GIA #status predicted
F;2-7,3-13/Disulfide bonds: #link GIC #status experimental
F;13/Modified site: anidated carboxyl end (Lys) (mide in mature form from following gly
F;15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
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                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-conotoxin GIA [validated] - cone shell (Conus geographus)
Nylternate names: alpha-CTX-GIA
NyContains: alpha-CTX-GIA
NyContains: alpha-CTX-GIA
NyContains: alpha-CTX-GIA
NyContains: alpha-CONOTOXIN GI
CSPECIES: Conus geographus (geography cone)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01782
R;Gray, W.R; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.
A;Riday, W.R; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.
A;Reference number: A92320; MUD:81191854; PMID:7014556
A;Accession: A01782
A;Molecule type: protein
A;Residues: 1-15 <GRA>
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C;Accession: A54534
R;Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
                                                                                                                                                                     Gaps
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F;2-7,3-13/Disulfide bonds: #status experimental F;13/Modified site: amidated carboxyl end (Cys) #status experimental
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A54534
heat-stable enterotoxin - Vibrio mimicus (fragment)
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Search completed: March 26, 2005, 17:25:59 Job time : 20.6786 secs
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A;Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-A;Reference number: A01824; MUID:86056320; PMID:4065341
                                                                                   C; Species: Vibrio cholerae
C; Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C; Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C; Accession: A41469; A01824; S34464; S34465; S34463; S34463
R; Astanan, S8, 3325-3329, H.; Nair, B.G.; Takeda, T.
Infect. Immun. S8, 3325-3329, 1990
A; Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio A; Reference number: A41469; MUID:90382953; PMID:2205577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 62-78 <TAK>
A; Experimental source: non-0:1 serovar
R; Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.;
PEBS Lett. 326, 83-86, 1993
A; Title: Purification and sequence determination of heat-stable enterotoxin elaborated
A; Reference number: S34463; MUID:93314823; PMID:8325391
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Fil9-6.1/Domain: propeptide #status predicted <PRO>
Fig-2-8/Product: heat-stable enterotoxin ST #status experimental <MAT>
Fi64-69,65-73,68-76/Disulfide bonds: #status predicted
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heat-stable enterotoxin ST precursor - Vibrio cholerae
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ive 0; Mismatches
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Molecule type: protein
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A; Residues: 1-78 <OGA>
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RESULT 14
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probable lysis protein S of prophage CP-933V Z3340 [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Spate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: D85845
Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Status: preliminary

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A; Molecule type: DNA
A; Moslecule type: DNA
A; Mossidues: 1-90 - 65TO-
A; Residues: 1-90 - 65TO-
A; Cross-references: UNIRPOT: Q8X4M8; GB.AE005174; NID: g12516391; PIDN: AAG57224.1; GSPDB:GA; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
A; Ge
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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March 26, 2005, 16:51:20 ; Search time 74.9821 Seconds (without alignments) 129.758 Million cell updates/sec Run on:

US-10-775-481A-2 19 score: Title: Perfect

1 NNTFYCCELCCNPACAGCY 19 Scoring table: Sequence:

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1612378 seqs, 512079187 residues Searched:

0 Word size :

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e summaries Post-processing: Listing first 45

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	P01559 escherichia	Q7m0u3 citrobacter	_	Q6veg7 escherichia	Q6veg8 escherichia	Q47185 escherichia	P07965 escherichia	-	•			P74977 yersinia en	•	•	•		Q9r578 vibrio chol	conus s	Q56643 vibrio chol	-	•			Q8x4m8 escherichia	Q7y2z2 stx1 conver	Q9t113 bacteriopha		Q8sc52 stx2 conver		0	Q8vui3 desulfovibr
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## ALIGNMENTS

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MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5; Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.; Moiwatani Of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli."; PEBS Lett. 215:165-170(1987).
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Okamoto K., Takahara M.;
"Synthesis of Bscherichia coli heat-stable enterotoxin STp as a pre-
pro form and role of the pro sequence in secretion.";
J. Bacteriol. 172:5260-5265(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE=85249571; PubMed=2990268; Sekizaki T., Akashi H., Terakado N.; Sekizaki T., Akashi H., Terakado N.; "Nuclocide sequences of the genes for Escherichia coli heat-stable enterotoxin I of bovine, avian, and porcine origins."; Am. J. Vet. Res. 46:909-912(1985).
                                                                                                                                                                                                                                   TRANSPOSON=Tn1681;
MEDLINE=81054703; PubMed=6254008;
So M., McCarthy B.J.;
"Nuclocide sequence of the bacterial transposon Tn1681 encoding a heat-stable (ST) toxin and its identification in enterotoxigenic Bscherichia coli strains.";
Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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J. Bacteriol. 172:5490-5493(1990).
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MEDLINE=94312375; PubMed=8038153;
                P01559; Q47653;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-2004 (Rel. 45, Last annotation update)
Heat-stable enterotoxin ST-IA/ST-P precursor.
72 AA.
PRT;
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MEDLINE-90368614; PubMed=2203756;
Dallas W.S.;
   STANDARD;
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SEQUENCE FROM N.A.
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DISULFIDE BONDS
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Sato T., Ozaki H., Hata Y., Kitagawa Y., Katsube Y., Shimonishi Y.; "Structural characteristics for biological activity of heat-stable enterotoxin produced by enterotoxingenic Escherichia coli: X-ray crystallography of weakly toxic and nontoxic analogs."; Biochemistry 31:8641-8650(1994).

-!-FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89108617; PubMed=2912902; MEDLINE=89108617; PubMed=2912902; MEDLINE=89108617; PubMed=2912902; M.R.; Citrobacter fraundii produces an 18-amino-acid heat-stable enterotoxin identical to the 18-amino-acid Escherichia coli heat-stable enterotoxin (ST Ia)."; Infect. Immun. 57:649-652(1989). PIR; A60103; A60103.
HSSP; P01559; IETN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Citrobacter freundii.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat-stable enterotoxin ST-IA/ST-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02048; Enterotoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
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                                                                                                                                                                                   epithelial cells.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the heat-stable enterotoxin family.
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hear-stable enterotoxin ST-Ia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> P (in Ref.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001489; Enterotoxin_HS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; V00612; CAA23883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; MS8746; AAA62776.1; -. EMBL; M25607; AAA24653.1; -. PIR; A01822; QHEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1ETL; X-ray; @=59-71.
PDB; 1ETM; X-ray; @=-.
PDB; 1ETN; X-ray; @=-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Conservative
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Matches 19; Conser
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PubMed=15364995;
PubMed=15364995;
PubMed=15364995;
Reischl U., Youssef M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
Real-time fluorescence PCR assays for detection and characterization of heat-labile I and heat-stable I enterotoxin genes from enterotoxigenic Escherichia coll.";
J. Clin. Microbiol. 43:4092-4100(2004).
EMBL; AY342057; AAQ92974.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009576; P:pathogenesis; IEA.
InterPro; IPR001489; Enterotoxin_HS; 1.
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PubMed=15364995;
Reischl U., Youssef M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
Reischl U., Youssecence PCR assays for detection and characterization of heat-labile I and heat-stable I enterotoxin genes from
                                                                                                                                                                                                                                         Gaps
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                   DB 2; Length 18; 4.7e-14;
GO, GO:0009405; P:pathogeneals; IEA.
InterPro; IPR001489; Enterotoxin_HS.
Pfam, PP02048; Enterotoxin_HS; 1.
PROSITE; P800273; ENTEROTOXIN H STABLE; 1.
SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Heat-stable enterotoxin ST-Ia (Fragment).
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Last annotation update)
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                                                                                                                                                              94.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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Enterobacteriaceae, Escherichia
                                                                                                                                                                                                                                                                                                  2 NTFYCCELCCNPACAGCY 19
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SEQUENCE FROM N.A.
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DISULFID
SEQUENCE
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PEPTIDE
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"Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Benefichia coli.",
J. Clin. Microbiol. 42.4092-4100(2004).
BMBL, AY342085, AA092975-1;
GO, GO:000576; C:extracellular; IEA.
GO, GO:0005405; P:pathogenesis; IEA.
Interpro, IRRO1409; Enterotoxin HS.
PROSITE; PS00273; ENTEROTOXIN HS; I.
                                                                                                                                                                                                                                                                                          Gaps
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                           Score 11; DB 2; Length 61;
Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                   61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JTL-2004 (TrEMBLrel. 27, Created)
05-JTL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Heat-stable enterotoxin ST ID (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin A2 precursor (STA2).
enterotoxigenic Escherichia coli.";
J. Clin. Microbiol. 42:4092-4100(2004).
EMBL; AY342059; AAQ92976.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001489; Enterotoxin.HS.
Pfam; PF02048; Enterotoxin.HS. 1.
PROSITE; PS00273; ENTEROTOXIN.H.STABLE; 1.
NON TER.
1 1 SEQÜENCE 61 AA; 6556 MW; 89788D3FAB3DCAOA
                                                                                                                                                                                                                             57.9%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                        11; Conservative
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108 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                  5 YCCELCCNPAC 15
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Best Local Similarity
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Q47185;
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SEQUENCE
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96 VEG
10 06 VEG
AC 06 VEG
DT 05 - J

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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SEQUENCE FROM N.A.

MEDLINE=89108616; PubMed=2643580;

MEDLINE=89108616; PubMed=2643580;

Guzman-Verduzio L.M., Kupersztoch Y.M.;

Guzman-Verduzio L.M., Kupersztoch Y.M.;

"Rectification of two Escherichia coli heat-stable enterotoxin allele sequences and lack of biological effect of changing the carboxy-terminal tyrosine to histidine.",

Infect. Immun. 57:645-648 (1989).

Infect. Immun. 58:645-648 (1989).

PUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells.

Infect. SUBCELLULAR LOCATION: Secreted.

Infect. SUBCELLULAR LOCATION: Column family.
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Moseley S.L., Hardy J.W., Hug M.I., Echeverria P., Falkow S.;
"Isolation and nucleotide sequence determination of a gene encoding a
heat-stable enterotoxin of Escherichia coli.";
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P07955; P26588;
01-AUG-1998 (Rel. 08, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-IB) (ST-H).
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Enterobacteriaceae; Escherichia.
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Heat-stable enterotoxin A2.
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D87850306E06E260 CRC64;
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Paden, PR00248; Enterotoxin HS; 1.
PROSITE; PS00273; ENTERQTOXIN_H_STABLE; 1.
Enterotoxin; Signal; Toxin.
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100.0%; Pre-
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MEDLINESSTORMS: PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5; MEDLINESSTORMS BY Y. Roizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.Y. Koizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.Y. Roizumi M., Hane M., Aimoto S., Takeda T., Mode of disulfide bond formation of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli."; PEBS Lett. 215:165-170(1987).

FEBS Lett. 215:165-170(1987).

FERS Lett. 215:165-170(1987).

Cyclase and increases cyclic GMP levels within the host intestinal
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Enterobacteriaceae, Escherichia.
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-!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
PIR; A01823; QHEC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=042:K86:H37 / 18D / ETEC;
MEDLINE=81264141; PubMed=7021541;
Chan S.-K., Glannella R.A.;
"Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pathogenic for man.";
J. Biol. Chem. 256:7744-7746(1981).
                       Heat-stable enterotoxin A3/A4.
                                                                                                                                                                                   DB 1; Length 72; 2.1e-05;
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1C5C9292BFCBA6BA CRC64;
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Pfam; PF02048; Enterotoxin_HS; 1.
Discr: PS0273; ENTEROTOXIN_H_STABLE; 1.
Direct protein sequencing; Enterotoxin; Toxin.
DISULPID
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Host-stable enterotoxin ST-2 (ST-B).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;

DWATSKARATH P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.,

Jagannatha H.M., Balganesh T.S.;

"Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escherichia coli.";

Gene 81:219-226(1999)."
                                                                                                                                                                                                                         MEDLINE-89108616; PubMed-2643580;
Guzman-Verduzio L.M., Kupersztoch Y.M.;
"Rectification of two Escherichia coli heat-stable enterotoxin allele
sequences and lack of biological effect of changing the carboxy-
terminal tyrosine to histidine.";
Infect. Immun. 57:645-648(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5; Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.; "Mode of disulfide bond formation of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli."; FEBS Lett. 215:165-170(1987).
                                                           MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L; Zhou X., Shen L.P., Chi C.W.; "Isolation and nucleotide sequence determination of a gene encoding heat-stable enterotoxin of Escherichia coll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90251166; PubMed=2187146; Rasheed J.K., Guzman-Verduzco L.M., Kupersztoch Y.M.; Two precursors of the heat-stable enterotoxin of Escherichia coli:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Amino-acid sequence of a heat-stable enterotoxin produced by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 54-72.
MEDLINE-83105138; PubMed-6759126;
Annoro S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y.,
Miwarani T.
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PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
Sirect protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19
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Infect. Immun. 39:1167-1174(1983)
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                                                                                                                                                           Toxicon 28:453-456(1990).
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                                                                                                                                                                                                                       STRAIN=86-11;
MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
Huang X., Yoshino K., Nakao H., Takeda T.;
"Nucleotide sequence of a gene encoding the novel Yersinia enterocolitica heat-stable enterotoxin that includes a pro-region-like sequence in its mature toxin molecule.";
Microb. Pathog. 22:89-97(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of a highly toxic, large molecular size heat-stable enterotoxin produced by a clinical isolate of Yersinia
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STRAIN=SERCYPE 0:3;
MEDLINE=95246644; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
Shimonishi Y.;
                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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Pfam; PF02048; Enterotoxin HS; 1.
PR0S1TB; PS00273; ENTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19
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                                   15-DEC-1998 (Rel. 37, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Heat-stable enterotoxin C precursor (Y-STC).
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(Rel. 26, Last sequence update)
(Rel. 44, Last annotation update)
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Heat-stable enterotoxin precursor.
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                                                                                                                Yersinia enterocolitica.
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               (Rel. 37, (Rel. 37, I
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69
72
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterocolitica.";
                                                                                                                                                                     NCBI_TaxID=630;
                   15-DEC-1998
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01-JUL-1993
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P31518;
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DISULFID
SEQUENCE
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HST_YERKR
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A PART THE THE TENT TO THE TEN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                            -I- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells (By similarity).
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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STRAIN=Serotype O:8;
MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
IDrahim A., Liesack W., Pike S., Stackebrandt E.;
"The polymerase chain reaction: an epidemiological tool to differentiate between two clusters of pathogenic Yersinia
Yerbinia kristensenii.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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Pred. No. 0.0044;
0; Mismatches 0; Indels
                                                                                                                                                                           STRAIN=1P490 / Serotype 0:12,25;
Ibrahim A., Liesack W., Stackebrandt E.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
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01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin A precursor (YST-A).
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By similarity.
By similarity.
By similarity.
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HSSP; P01559; IETN.
InterPro; IPR001489; Enterotoxin HS.
PFam; PF02048; Enterotoxin HS; 1.
PROSTIE; PS00273; ENTEROTOXIN HS; 1.
Enterotoxin; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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Enterobacteriaceae, Yersinia.
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66
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63
7068 MW;
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                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                       NCBI_TaxID=28152;
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guanylate intestinal

Yersinia

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                                                                                                                                                                                        Microb. Pathog. 23:189-200(1997).
-!- FUNCTION: Toxin which activates the particulate form of guanyla cyclase and increases cyclic GMP levels within the host intesti epithelial cells. Could play an important role in pathogenesis.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
STRAIN=84-50 / Serotype 0:5;
MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
Maruyama T., Fukushima H., Takeda T.;
"The novel heat-stable enterotoxin subtype gene (ystB) of Yersin
enterocolitica: nucleotide sequence and distribution of the yst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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GAZYW W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.;
"Peptide toxins from Conus geographus venom.";
J. Biol. Chem. 256:4734-4740(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9; DB 1; Length 71;
Pred. No. 0.0047;
0; Mismatches 0; Indels
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P01519;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-conotoxin GIA [Contains: Alpha-conotoxin GIA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxin B.
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PROSITE; PS0273; ENTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19
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By similarity.
By similarity.
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52
71
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68
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7670 MW;
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Best Local Similarity 10v.v.
Best Local Similarity
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                                                                                                                                                                       genes.";
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CXAA_CONGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted.
INDUCTION: In cultured cells, expressed only at temperatures <30 degrees Celsius. Under conditions of high osmolarity and alkaline pH (as it is the case in the host's intestine), it is expressed at
                                                           encoding
                                                                                                                                                                                           SEQUENCE OF 54-71.
MEDLINE=86004705; PubMed=4043080;
Takao T., Tominaga N., Yoshimura S., Shimonishi Y., Hara S., Inoue T.,
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Enterobacteriaceae, Yersinia.
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MEDLINE=90354067; PubMed=2201642;
Delor I., Kaeckenbeeck A., Wauters G., Cornelis G.R.;
"Nucleotide sequence of yst, the Yersinia enterocolitica gene
the heat-stable enterotoxin, and prevalence of the gene among
pathogenic and nonpathogenic yersiniae.";
Infect. Immun. 58:2983-2988(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 degrees Celsius.
SIMILARITY: Belongs to the heat-stable enterotoxin family.
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PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
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022F99B3800C861B CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 44, Last annotation update)
Heat-stable enterotoxin B precursor (Y-STB).
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By similarity.
By similarity.
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100.0%; Pred. No. 0.0
Live 0; Mismatches
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InterPro; IPR001489; Enterotoxin_HS.
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Best Local Similarity 100....
Conservative
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71 AA;
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DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI

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                      Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C., Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M., Cruz L.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Braun W., Go N.;
"Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations."; Biochemistry 28:4853-4860(1989).
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MEDLINE=98321613; PubMed=9660176;
Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;
"Two distinct structures of alpha-conotoxin GI in aqueous solution.";
Eur. J. Biochem. 254:238-247(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Groebe D.R., Gray W.R., Abramson S.N.;
"Determinants involved in the affinity of alpha-conotoxins GI and SI
"for the muscle subtype of nicotinic acetylcholine receptors.";
Biochemistry 36:6469-6474 (1997).
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MEDLINE-95349531; PubMed=7623764;
Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;
Groebe D.R., Dumm selectively inhibit one of the two acetylcholine binding sites of incortinc receptors.";
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MEDLINE-89352562; PubMed-2765514;
Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
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MEDLINES-96378624; PubMed=8784187; DOI=10.1021/bi960820h;
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"Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
                                                                                           "Conotoxin GI: disulfide bridges, synthesis, and preparation of
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Pardi A., Galdes A., Florance J., Maniconte D.;
"Solution structures of alpha-conotoxin G1 determined by two-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS OF ARG-9.
MEDLINE-97317090; PubMed-9174364; DOI=10.1021/bi970195w;
MEDLINE=84280842; PubMed=6466616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 35:11329-11335(1996)
                                                                                                                    iodinated derivatives.";
Biochemistry 23:2796-2802(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dimensional NMR spectroscopy.";
Biochemistry 28:5494-5501(1989)
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15 Alpha-conotoxin GIA.
13 Alpha-conotoxin GI.
Biochemistry 38:11895-11904 (1999).

-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (MAChR) and thus inhibit them. The higher affinity site for alpha-conotoxin GI is the alpha/delta site on mouse muscle-deriverd BC3H-1 receptor, an the other site (alpha/gamma site) on nicotinic receptors from Torpedo californica electric organ.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
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Lysine amide (in alpha-conotoxin GIA)
R->A: Reduction in affinity for both
alpha/delta and alpha/gamma sites on
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Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure; Acetylcholine receptor inhibitor; Amidation;
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PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence updator)
01-UN-2003 (TrEMBLrel. 24, Last annotation updator)
01-ST-1, NAG-ST, VM-ST=HEAT-stable enterotoxin.
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100.0%; Pred. No. 4.9;
tive 0; Mismatches
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001489; Enterotoxin_HS.
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1628 MW;
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1QS3; NMR; A=2-13.
1XG3; NMR; @=1-14.
1XGB; NMR; @=1-14.
1XGC; NMR; @=1-14.
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A01782; NTKNAG.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-ST-2, VC-H-ST=HEAT-stable enterotoxin.
Vibrio cholerae.
Bacteria; Protecbacteria; Gammaprotecbacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TAXID=666;
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The peptides of the invention can be used in a vaccine useful for conferring protection against diarrhoes. They may also be used in a diagnostic or reagent system for assaying for infections caused by t B.coli strains. (Updated on 25-MAR-2003 to correct PA field.)
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Aay40509 ST recept
Aay3994 E. coli S
Ade10846 Chimeric
Adm39751 Escherich
Ady73480 Escherich
Ady73480 Escherich
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Ady331 E. coli S
Adr4833 E. coli S
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15 83.3 15 2 AAR85968 15 83.3 15 2 AAR85968 15 83.3 15 2 AAR40525 15 83.3 15 2 AAR405304 15 83.3 15 8 ADR45839 15 83.3 18 8 ADR45839 15 83.3 18 7 ADE10847 15 83.3 18 7 ADE10847 15 83.3 18 8 ADP73481 15 83.3 18 8 ADP73481 16 77.8 14 2 AAR85969 14 77.8 14 2 AAR85969 14 77.8 14 2 AAR85969 14 77.8 14 2 AAR93983 14 77.8 14 2 AAR93983 14 77.8 14 2 AAR93983 16 77.8 14 7 ADE10845 17.8 14 77.8 14 8 ADG63945 18 77.8 14 7 ADE10845 19 77.8 14 7 ADE10845 10 77.8 14 8 ADG63945 11 77.8 14 8 ADG63945 11 77.8 14 8 ADG63945 12 77.8 14 8 ADG63945 13 77.8 14 8 ADG63945 14 77.8 14 8 ADG63945 14 77.8 14 8 ADG63945 15 83.3 83WO-US002008. 10 SCRIPPS CLINIC & RES FOUND. 11 SCRIPPS CLINIC & RES FOUND. 12 SCRIPPS CLINIC & RES FOUND. 13 SCRIPPS CLINIC & RES FOUND. 14 189753/30. 15 AAR939669 16 ABR753/30. 17 SCRIPPS CLINIC & RES FOUND. 18 ABR353/30.	Aar85968 ST 1* rec Aar85963 ST 1* rec Aay40525 ST recept Adr45844 Amino aci Adr45844 Amino aci Adr45849 B. coli a Adr39752 Bscherich Adg63947 Chimeric Add39752 Bscherich Adg63947 E. coli S Aar85969 ST 1* recept Aar865969 ST recept Aar86569 ST recept Aar865969 ST recept Aar86569 ST recept Aar	-stable Escherichia coli enterotoxin en.	). igenicity of E.coli enterotoxin - useful and for diagnostic tests.
15 83.3 15 2 15 2 15 2 15 8 3.3 15 2 15 8 3.3 15 2 15 8 3.3 15 2 15 8 3.3 15 2 15 8 3.3 15 2 15 8 3.3 15 15 8 3.3 18 15 8 3.3 18 18 15 8 3.3 18 18 14 17.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 77.8 14 8 14 8 14 8 14 8 14 8 14 8 14 8 14	AAR85968 AAR40525 AAY40525 AAY40526 AAY40530 ADR45839 ADR10847 ADM39752 ADG63947 ADG63947 AAR85964 AAR85964 AAR85969 AAX40531 AAX40530 AAX40530 AAX40530 AAX90526 AAX90526 AAX90526 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX90530 AAX905	18 AA. tic heat s; antig	    FOUNI .h ant: .rhoea
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The invention relates to a conjugated compound that comprises a ST (heatstable toxin) receptor moiety selected from one of the sequences shown in AAV40508-Y40559 and an active moiety (antisense molecule). The compound is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells. The present sequence represents the amino acid sequence of a ST receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic, hepadnavirus nucleocapsid protein, hepatitis B core, HBc,
vaccine, B cell epitope, T cell epitope, immunostimulant.
                                                                                                                                                                                                                                                                                                      Conjugated compound comprising a receptor moiety and active moiety, useful for the treatment/prevention of colorectal cancer.
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Pred. No. 1.3e-12;
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22-AUG-2000; 2000US-0226867P.
15-AUG-2001; 2001US-00930915.
                                                                                                                         95US-00467920.
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Best Local Similarity 100.
Matches 18; Conservative
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                  Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide ST I*
                                                                                                                                                            26-OCT-1993;
                                                                                                                          06-JUN-1995;
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                                                  US5962220-A.
                                                                                       05-OCT-1999
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                                                                                                                                                                                                                                   Waldman SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New conjugated compounds are provided which consist of (1) an ST receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding molety and (2) an active molety which is a radio- stable agent.

ST. refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitcmycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastissed tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                                                                                                                                                                                ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer; colorectal; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugated cpds, which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.
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                                                                                                                         AAR85947 standard; peptide; 18 AA
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                  AAY40509 standard; peptide; 18
NTFYCCELCCYPACAGCN 18
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94US-00305056.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                          WO9511694-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1993;
                                                                                                                                                                                             19-JAN-1996
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                                                                                                                                                            AAR85947;
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Matches

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WPI; 2003-852775/79.

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The invention relates to a recombinant hepadnavirus nucleocapsid protein, i.e. a chimeric hepatitis B core (HBC) protein (1), displaying one or more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or C-terminus, or having a heterologous linker for a conjugated epitope in C-terminus containing a Cys residue at, or near, the C-terminus that confers enhanced stability to the particles. A vaccine comprising (1) is useful for inducing an immune response in an inoculated host animal, by inoculated animal with the vaccine, and maintaining that inoculated animal for a time period sufficient for that animal, by inoculated animal for a time period sufficient for that animal to develop an immune response. The immunogenic particles formed using (I) are substantially free of binding to nucleic acids, and are most stable than the particle formed from otherwise identical HBc chimer that lacks the creatidue. The chimer particles are most seable on storage in aqueous compositions that are particles are most estable on storage in aqueous compositions that are particles are most estable on storage in aqueous compositions that are particles are most exhibits the self-assembly not excellent B cell and T cell immunogenicities. The chimer particles are often far more immunogenic than the similar conjugates that lack a C-terminal Cys. Immunogenic than the similar conjugates that lack a C-terminal Cys. Immunogenic than similar particles assembled from the chimer molecules are enhanced as compared to similar particles assembled from chimer molecules are enhanced as compared to similar particles and main of the invention acides and near the invention acides and near the invention acides and near the invention of the inve
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Novel recombinant hepadnavirus nucleocapsid protein, termed as chimeric hepatitis B core protein, displays immunogenic epitopes at N-terminus, HBc immunogenic loop with linker for conjugated epitope and C-terminus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 5; Length 18; 100.0%; Pred. No. 1.3e-12; ive 0; Mismatches 0; Indels
                                                                                                 Disclosure; Page 38; 289pp; English.
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ADE10846
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21-FEB-2002; 2002US-00080299, 21-FEB-2002; 2002US-00082014, 21-FEB-2003; 2003US-00372076

Friede M; PAGE M. FRIEDE M.

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                                                                                                                                                             The invention describes a method of treating chronic hepatitis comprising administering to a patient a T cell-stimulating amount of a vaccine comprising immunogenic particles dissolved or dispersed in a diluent, where the immunogenic particles desconsists of recombinant hepatitis B core (HBC) chimeric protein molecules, and maintaining the patient to induce T cinvention are useful for treating chronic hepatitis B infection. This is the amino acid sequence of a chimeric hepatitis B infection. This is the amino acid sequence of a chimeric hepatitis B infection. This is epitope useful for expression within the HBV chimer at the N-terminus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant chimer avian hepatitis B core protein molecule, useful as an immunogen for inducing a B cell or T cell response to produce antibodies, or as a vaccine against pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel recombinant immunogenic chimeric avian hepatitis B core (AHBc) nucleocapsid proteins. Specifically, it refers to an AHBc protein that has been engineered to display an immunogenic B cell or I cell epitope, exhibit enhanced stability and an absence of nucleic acid binding as a self assembled particle. The present invention describes the chimeric AHBc protein as truncated at the C-terminus and
                                 Treating chronic hepatitis B infection by administering a T cell-
stimulating vaccine containing immunogenic particles having recombinant
carboxy-terminal truncated hepatitis B core (HBC) chimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic; avian hepatitis B virus; nucleocapsid;
self assembled particle; immunogen; inoculum; vaccine; immunostimulant;
antibacterial; virucidal; B-cell epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                             Disclosure; SEQ ID NO 80; 111pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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Best Local Simil
Matches 18; C
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stability in aqueous solution, an increased yield and more immunogenicity than similar conjugates that lack N- or C-terminal cysteines. Furthermore, a reduction in the number of positively charged residues Furthermore, a reduction in the number of positively charged residues (lysine and arginine) towards the C-terminus prepares self-assembled particles that are substantially free of nucleic acid binding. As such, these chimeric particles can be used as immunogens of an inoculum that induce a B cell or T cell response in an animal to produce antibodies. It can also be useful for developing a vaccine to, protect against the pathogen from which the heterologous epitope or the hapten is derived. Accordingly, these compositions exhibit immunostimulant, antibacterial and virucidal activities. This peptide sequence is an exemplary B-cell epitope peptide immunogen useful for both linkage to the linker residue after expression of a contemplated chimer and for expression within an containing introduced cysteine residues that confers an enhanced HBc chimer of the invention 88888888888888888888888888

Sequence 18 AA;

Length 18; 100.0%; Score 18; DB 7; Length 18 100.0%; Pred. No. 1.3e-12; ive 0; Mismatches 0; Indels 18 1 NTFYCCELCCYPACAGCN Query Match 100. Best Local Similarity 100. Matches 18; Conservative g ઠે

ADG63946 standard; peptide; 18 AA. ADG6394

ADG63946; 

Recombinant chimer hepatitis B core protein immunogenic epitope #71.

(first entry)

11-MAR-2004

Recombinant chimer hepatitis B core protein; HBc; immunogenic epitope; HBc immunodominant loop; immune response.

Escherichia coli.

02-OCT-2003.

US2003185858-A1

21-FEB-2002; 2002US-00082014.

15-AUG-2001; 2001US-00930915.

(BIRK/) BIRKETT A J.

Birkett AJ;

WPI; 2004-031988/03.

preparing Recombinant chimer hepatitis B core protein molecule useful for preparir vaccine or inoculum includes peptide-bonded heterologous immunogenic epitope at N-terminus in the hepatitis B core immunodominant loop or Cterminus of the chimer.

Disclosure; SEQ ID NO 79; 110pp; English.

The invention relates to a recombinant chimer hepatitis B core (HBC) protein molecule that includes a peptide-bonded heterologus immunogenic epitope at the N-terminus in the HBC immunodominant loop or the C-terminus of the chimer, or a heterologous linker residue for a conjugated epitope present in the loop. The invention also relates to an immunogenic particle comprising the recombinant hepatitis B core chimeric protein molecules, a vaccine comprising the immunogenic particles dissolved or dispersed in a diluent, a nucleic acid that encodes a recombinant HBC protein molecule or its variant, analogue, or complement and a method for inducing an immune response in an inoculated host animal comprising

animal for a period of time sufficient to enable development of an immune response. The recombinant chiner hepatitis B core protein molecule is used in an immunogenic particle for preparing a vaccine useful for inducing an immune response in an inoculated host animal. This sequence represents an HBc protein immunogenic B cell epitope of the invention. inoculating a host animal with a vaccine and maintaining the inoculated 8888888

Sequence 18 AA;

Gaps ö Length 18; Indels .; 0 Score 18; DB 8; Pred. No. 1.3e-12; Mismatches ; Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0

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1 NTFYCCELCCYPACAGCN 18

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RESULT

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Gaps

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ADP73480 standard; peptide; 18 AA.

ADP73480;

(first entry) 09-SEP-2004

Escherichia coli B cell epitope of gene ST, SEQ ID 93.

transgenic animal; Hepatitis B virus nucleocaspid core protein; HBc; enhanced stability; hepatotropic; virucide; immunology; protein engineering; immunogen; vaccine; Hepatitis B infection

Escherichia coli.

WO2004053091-A2.

24-JUN-2004

10-DEC-2003; 2003WO-US039164.

10-DEC-2002; 2002US-0432123P.

(APOV-) APOVIA INC

Haron JA; Birkett AJ, Lyons K,

ü New recombinant chimer hepatitis B core (HBc) protein molecules useful the fields of immunology and protein engineering, in particular as an immunogen in a vaccine for Hepatitis B infections.

Disclosure; SEQ ID NO 93; 338pp; English

The invention relates to a novel recombinant chimeric Hepatitis B virus nucleocaspid (core) protein (HBC), up to 600 or 380 amino acid residues in length. The chimeric protein is engineered for both enhanced stability of self-assembled particles and the substantial absence of nucleic acid binding by the particles. The invention further comprises: a recombinant HBC protein chimeric molecule that has a length of 135-365 amino acid residues and contains four peptide-linked amino acid residue sequence comparis from the N-terminus that are denominated Domains I, II, III and IV. The invention also provides nucleic acids, polypeptides, host cells, vectors and transgenic animals used in the methods of the invention. The chimeric compositions of the invention have hepatotropic and virucide activities. The methods and compositions of the present invention are useful in the fields of immunology and protein engineering, in particular for using a chimeric hepatitis B virus nucleocapsid protein as an immunogen in a vaccine for Hepatitis B infections. This sequence represents a Hepatitis B virus nucleocapsid core) protein related 

Sequence 18 AA;

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The invention relates to treating chronic hepatitis, by administering a vaccine comprising immunogenic particles having recombinant hepatitis B core (HBC) chimeric protein molecules (where truncated Hbc molecules are linked N-terminally or C-terminally to an immunogenic epitope), that stimulate T cell production, to a patient chronically infected with hepatitis B virus, and maintaining patient for time sufficient to induce T cells activated against HBC. The chimeric proteins are still capable of the patitis B virus, and maintaining patient for time sufficient to induce T cells activated against HBC. The chimeric proteins are still capable substantially free of binding to nucleic acids, and the particles display chanced stability. Also included is enhancing (M2) the production of one or more of gamma-producing CD8+, CD4+ T cells and cytotoxic T lymphocytes against hepatitis B virus, involving administering to a patient chronically infected with hepatitie B virus, a T cell-stimulating amount of a vaccine comprising immunogenic particles dissolved or dispersed in a ciluent containing one or both of an agonist of toll-infe receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising HBC chimeric protein molecules and maintaining the patient for a sufficient time to induce T cells activated against HBC. The immunogenic epitopes containing a patient chronically infected with hepatitis B virus, the
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                                                                                                                                                                                                                                                                                                                                                                  HBV; chronic hepatitis; HBc; nucleocapsid core protein; vaccine; immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; cD4+ cell; cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating chronic hepatitis, by administering vaccine comprising mimunogeniac particles having recombinant hepatitis B core chimeric protein molecules, that stimulates T cell, to patient chronically infected with hepatitis B virus.
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                    Length 18;
                                                       0; Indels
                 Score 18; DB 8; L
Pred. No. 1.3e-12;
                                                         Mismatches
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100.0%; Sc.
100.0%; Pre
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                                                                                                                                                                                                                     ADR12773 standard; peptide; 18
                                                                                         1 NTFYCCELCCYPACAGCN 18
                                                                                                                E. coli ST B cell epitope #2.
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21-FEB-2003; 2003US-00372076.
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                                                                                                                                                                                                                                                                                              (first entry)
               Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           TLR-4; TLR-9; epitope
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FRIEDE M.
SCHMIDT A E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified peptide (PI) capable of activating the guanylate cyclase C (GC-C) receptor. Further disclosed is a pharmaceutical composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastrointestinal disorder is gastrointestinal metlity disorder, is gastrointestinal metlity disorder, irritable bowel syndrome, chronic constipation, a functional gastrointestinal metlity disorder, irritable bowel syndrome, chronic constipation, a functional gastrointestinal disorder, gastroesophageal reflux disease, functional gastroparesis, chronic intestinal dyspepsia, nonlock dyspepsia, agastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified peptide capable of activating the guanylate cyclase (
receptor, useful for treating obesity, congestive heart failure and
present sequence is a B cell epitope suitable for inclusion in the chimeric protein of the invention.
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                                                                                                                                              0; Indels
                                                                                                    100.0%; Score 18; DB 8; I
100.0%; Pred. No. 1.3e-12;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                          ADR48343 standard; peptide; 18 AA
                                                                                                                                                                                         1 NTFYCCELCCYPACAGCN 18
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15-MAY-2003; 2003US-0471288P.
12-NOV-2003; 2003US-0519460P.
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                                                                                                    Query Match
Best Local Similarity 100.'
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial ST peptide #4.
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                                                              Sequence 18 AA;
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disease. The peptide of the invention is also useful for treating obesity, congestive heart failure, cystic fibrosis or a patient suffering from constipation. The PI/GCC receptor agonist is useful for treating cancer, respiratory disorder, neurological disorder, disorder associated with carbonate imbalance, erectile dysfunction, insulin-related disorder or inner ear disorder. Pl is useful in treating slow digestion or alow stomach emptying. Pl is useful in relieving symptoms of gastroparesis stomach emptying or preventing asthma, nephritis, hepatitis, the sucception or preventing asthma, nephritis, hepatitis, planceatitis, allergies, etc. Pl is useful for treating or preventing type II diabetes mellitus, hyporglycaemia, respiratory disorders including inhalation. Pl is useful for treating or preventing represently nephropathy and edema formation. Pl is useful for treating or preventing haddech, anxiety, sleep disorders and memory loss. Pl is useful as a marker to identify, detect, stage, or diagnosis diseases and conditions of the small intestine, including Crohn's disease, onlits, inflammatory bowel disease, tumours, etc. Pl can be conjugated to diagnostic or therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic throats lesions and specific cells lining the intestinal tract, thus useful in targeting radioactive moleties or therapeutic moieties to the intestine to aid in imaging and diagnosing or treating contesting to the colorectal/metratasised or local colorectal cancer. The current sequence representes a bacterial ST peptide which is an activator of the GC-C receptor. ST peptide are considered super agonists of GC-C and are very resistant to proteolytic degradation. 

Sequence 18 AA;

Gaps ö 100.0%; Score 18; DB 8; Length 18; 100.0%; Pred. No. 1.3e-12; ive 0; Mismatches 0; Indels 1 NTFYCCELCCYPACAGCN 18 Query Match
Best Local Similarity 100.0%;
Marches 18; Conservative 0 ઠે

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1 NTFYCCELCCYPACAGCN 18

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ADR48331 standard; peptide; 18 AA.

ADR48331;

04-NOV-2004 (first entry)

E. coli ST I* peptide.

Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer; anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory; neuroprotective; vasctropic; auditory; antiementic; antiatethmatic; nephrotective; vasctropic; utilicory; imminementic; antiallergic; antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic; antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder; irritable, bowel syndrome; constipation; gastroophageal reflux disease; heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis; inflammatory bowel disease; obesity; heart failure; cystic fibrosis; cancer; respiratory disorder; neurological disorder; carbonate imbalance; erectile dysfunction; inner ear disorder; slow digestion; nausea; vomiting; bloating; aschma; nephritis; hepatitis; pancreatitis; allergy; retinopathy; nephropathy; sleep disorder. 

Escherichia coli.

WO2004069165-A2

19-AUG-2004.

28-JAN-2004; 2004WO-US002390

28-JAN-2003; 2003US-0443098P. 15-MAY-2003; 2003US-0471288P. 12-NOV-2003; 2003US-0519460P.

(MICR-) MICROBIA INC. 

Currie MG, Mahajan-Miklos S;

WPI; 2004-604332/58.

Novel purified peptide capable of activating the guanylate cyclase Creceptor, useful for treating obesity, congestive heart failure and benign prostatic hyperplasia.

Disclosure; Page 28; 93pp; English.

The invention relates to a purified peptide (P1) capable of activating the guanylate cyclase C (GC-C) receptor. Further disclosed is a the guanylate cyclase C (GC-C) receptor. Further disclosed is a composition comprising the peptide of the invention. The composition of the invention is useful for treating a gastrointestinal disorder, which involves administering P1, where the gastrointestinal disorder, gastrointestinal motility disorder, irritable bowel syndrome, chronic constipation, a functional constrabur, dyspepsia, functional dyspepsia, nonuleer dyspepsia, constrabur, dyspepsia, functional dyspepsia, nonuleer dyspepsia, gastroparesis, functional disorder, gastroparesis, constrainal pseudo-obstruction, colonic pseudo-obstruction, colonic pseudo-obstruction, colonic pseudo-obstruction, colonic pseudo-obstruction, colonic pseudo-obstruction, constipation. The P1/GC-c receptor agonist is useful for treating obstruction the P1/GC-c receptor agonist is useful for treating cancer, respiratory disorder, neurological disorder, disorder associated with carbonate imbalance, erectile dysfunction, insulin-related disorder cor inner ear disorder. Pl is useful in treating show diseatoparesis such as nausea, vomitting, bloating, and delayed gastric emptying. Pl is useful for treating or preventing than an ausea, vomitting, bloating, and delayed gastric emptying. Pl is useful for treating inhalation. Pl is useful for treating or preventing treating inhalation. Pl is useful for treating retinopathy, chapters, and edema formation. Pl is useful for treating or preventing treating inhalation. Pl is useful for treating or preventing the maxiety, saleed disorder and memory loss. Pl is useful confused to disposed or the small intestine, including Crohn's disease, colitis, inflammatory confused by the small intestine, including Crohn's disease, colitis, inflammatory useful in transition and peculistical colls bearing of the amenial in transition are and expectition and expectition and expectition and expectition and peculisticals useful in targeting radioactive moieties or therapeutic moieties to the intestine to aid in imaging and diagnosing or treating colorectal/metastised or local colorectal cancer. The current sequence represents a bacterial ST peptide which is an activator of the GC-C receptor. ST peptides are considered super agonists of GC-C and are very to proteolytic degradation. receptor. ST resistant to

Sequence 18 AA;

Gaps ö Length 18; Ouery Match 100.0%; Score 18; DB 8; Length 18 Best Local Similarity 100.0%; Pred. No. 1.3e-12; Matches 18; Conservative 0; Mismatches 0; Indels

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1 NTFYCCELCCYPACAGCN 18

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RESULT 12

ADR45823 standard; peptide; 18 AA.

ADR45823;

(first entry) 18-NOV-2004

heat stable toxin; ST; ST receptor; colorectal cancer; gastric cance; oesophageal cancer; colorectal cell; gastric cell; oesophageal cell; ST Ia. ADR45823
ID ADR4
XX AC ADR4
XX DF 18-1
XX DE Amti
XX W hea
KW hea
KW ST

Amino acid sequence of peptide ST I* inhibiting ST activity.

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The inventors claim peptides of formula (P)n (see FT; see also AAP30263) having 4n-18n amino acids and pref. being laevorotatory (where n is 1 or 2). In AAP30262 and AAP30263, N=2. When n is 2, the peptide comprises two peptide sequences P, which may be the same or different, each having 4-18 amino acids chosen from the peptide P SQ in AAP30262 or AAP30263. The two F sequences may be joined (a) by a disulphide bond or (b) by a bond formed between a carboxyl gp. of one sequence of an amino gp. of the other. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                   Peptide(s) used to vaccinate against E. coli enterotoxin(s) - contg. e.g. asparagine threonine phenylalanine tyrosine cysteine cysteine glutamic acid leucine cysteine cysteine asparagine sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
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100.0%; Pred. No. 2.1e-12;
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                                                                                                                                                          Boquet P;
                                                                                                                                                                                                                                                                                                                    Claim 1; Page 40; 50pp; French
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                  83EP-00400827
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94US-00305056,
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                                                                                             (INSP ) INST PASTEUR.
(CNRS ) CENT NAT RECH
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                                                                                                                                                                                             WPI; 1983-816301/46.
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                                                    26-APR-1982;
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                  26-APR-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waldman SA;
                                                                                                                                                          Tartar A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR85966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stable toxin (ST) receptor molecules on the surface of a merastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 mh of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the number of ST receptor molecules on the surface of the cancer cell is increased. Therapeutic compositions comprising components which target ST receptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that have diseases that affect colorectal, gastric and coesophageal cells, including colorectal, gastric or oesophageal cancers. The present sequence represents a peptide which inhibits ST activity, and is designated ST I* It is used as the ST receptor ligand in the method
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                                                                                                                                                                                                                                                                                                                        Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification describes a method for increasing the number of heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of peptide used to vaccinate against E. coli enterotoxin(s).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                          Wolfe HR;
                                                                                                                                                                                                                                                          Schulz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine, enterotoxin; diaorrhoea; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID NO 3; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP30263 standard; peptide; 36 AA.
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/label= Peptide P
                                                                                                                                                                                                                                                        Pitari GM, Park J,
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                                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                   10-FEB-2004; 2004WO-US003765.
                                                                                                                                                                          10-FEB-2003; 2003US-0446730P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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1es 18; Conservative
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                                                                                                                                                                                                                                                                                             WPI; 2004-615913/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
                                                      WO2004071436-A2.
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                Unidentified.
                                                                                                                                                                                                                                                     Waldman SA,
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25-APR-1992
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RESULT 13 AAP30263

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Matches

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Gaps

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Length 36; 0; Indels

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New conjugated compounds are provided which consist of (1) an ST receptor binding molety and (2) an active molety which is a radio- stable agent. 'ST' refers to a heat stable toxin produced by B.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New conjugated compounds are provided which consist of (1) an ST receptor binding moiety and (2) an active moiety which is a radio- stable agent. 'ST refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer; colorectal; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugated cpds, which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.
                                                                                                                                                                                                                                   94.4%; Score 17; DB 2; Length 17; 100.0%; Pred. No. 1.5e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR85961 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ST I* receptor ligand portion.
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                                                                                                                                                                                                                                                                                                           2 TFYCCELCCYPACAGCN 18
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94US-00305056.
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                   Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1994;
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AAR85961
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94.4%; Score 17; DB 2; Length 17; 100.0%; Pred. No. 1.5e-11; iive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 17, Conservative

Query Match

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1 NTFYCCELCCYPACAGC 17
               1 NTFYCCELCCYPACAGC 17
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Search completed: March 26, 2005, 17:20:57 Job time: 80.0357 secs

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Gaps

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Sequence Seq

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

Database :

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Sequence 3, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
TITLE OF INVENTION: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
STATE: Pennsylvania
COUNTRY: One Liberty Place - 46th Floor
CITY: ADDRESSEE - MOGOCK WASHBURD - 46th Floor
CITY: ADDRESSEE - MOGOCK WASHBURD - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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Pred. No. 2.8e-13;
; Mismatches 0;
US-09-138-237A-19
US-09-138-237A-24
US-08-141-892A-25
US-08-18-47A-20
US-08-583-447A-25
US-08-467-920-25
US-08-467-920-25
US-08-655-930-25
US-09-193-997-20
US-09-138-237A-25
US-09-138-237A-25
US-09-138-237A-25
US-09-138-237A-25
US-09-138-237A-25
US-09-138-237A-25
US-09-138-237A-21
US-08-141-892A-21
US-08-141-892A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION TATA:
APPLICATION NUMBER:
FILING DATE: ATTORNEY, AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECHONE: 215-568-3190
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Matches 18; Conserv
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Sequence 3,
Sequence 18,
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. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-53-447A-3
US-08-635-930-3
US-09-139-997-3
US-09-138-237A-3
US-08-141-892A-18
US-08-141-892A-18
US-08-141-892A-18
US-08-447A-23
US-08-467-920-18
US-08-635-930-23
US-08-635-930-23
US-08-635-930-23
US-09-138-237A-18
US-09-138-237A-18
US-09-138-237A-23
US-08-141-892A-24
US-08-141-892A-24
US-08-583-447A-19
US-08-141-892A-24
US-08-18-237A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513545 seqs, 74649064 residues
                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                               Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                  1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                            US-10-775-481A-3
18
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \begin{array}{c} 0.001 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\ 0.000 \\
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Gaps

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Sequence 3, Application US/08635930

Patent No. 6060037

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: Compositions That Specifically Bind To

TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using

TITLE OF INVENTION: The Same

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris

STRET: Den Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Worderfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE: A-CCT-1993
CLASSIFICATION NUMBER: 08/141,892
FILING DATE: A-CCT-1993
CLASSIFICATION NUMBER: 13,229
FILING DATE: A-CCT-1993
CLASSIFICATION NUMBER: 33,229
ATPORNEY/AGENT INFORMATION:
MAME: Defluca, Mark
REGISTRATION NUMBER: 33,229
FELEPHONE: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,930
FILING DATE: 26-APR-1996
CLASSIPICATION NUMBER: 08/141,892
FILING DATE: 26-CCT-1993
CLASSIPICATION: 435
FILING DATE: 26-CCT-1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIPICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NTFYCCELCCYPACAGCN 18
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                                                                                                                           Sequence 3 Application US/08583447A

Fatent No. 5879656

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

ITLE OF INVENTION: ST Receptor Binding Compounds and

ITLE OF INVENTION: Methods of Using the Same

CORRESPONDENCE ADDRESS:

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels
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US-08-467-920-3
US-08-467-920-3
Sequence 3, Application US/08467920
FRETCH NO. 596220
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically TITLE OF INVENTION: Bind TO Colorectal Cancer Cells TITLE OF INVENTION: Bind TO Colorectal Cancer Cells TITLE OF INVENTION: And Methods Of Using The Same NUMBER OF SEQUENCES: 54
CORRESPONDENCES. 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STEET: One Liberty Place, 46th Floor CITY: Philadelphia STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USAN
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLIASSIFTCATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE 215-568-3100
TELEPHONE 215-568-3100
TELEPHONE 215-568-3100
TELEPHONE 215-568-3100
TELEPAX: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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1 NTFYCCELCCYPACAGCN 18
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                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09193997
Patent No. 6087109
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 608710918
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
CITY: Philadelphia
                                                                                                                                                                                                                                Lucty match
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1589
TELECHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
                        TJU-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
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APPLICATION NUMBER: 08/467,920
FILING DATE:
REGISTRATION NUMBER: 33,229
REFERNICE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                       1 NTFYCCELCCYPACAGCN 18
     33,229
                                                                                                                                TYPE: amino acid:
; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-635-930-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Best Local Similarity 100.0
Matches 18, Conservative
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STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-09-193-997-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-193:997-3
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Gaps
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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Patent No. 551888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
                                           GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
; Sequence 3, Application US/09138237A; Patent No. 6268159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: FRNGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-09-138-237A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
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Gaps

Gaps

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Query Match 94.4%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 3.3e-12; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   2 TFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                1 TFYCCELCCYPACAGCN 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                 US-08-141-892A-23
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                                                               TOPOLOGY:
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Philadelphia
STATE: Philadelphia
STATE: Philadelphia
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 551888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.4%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 3.3e-12; Matches 17; Conservative 0; Mismatches 0; Indels
MEDIUM TYPE: 3.5 inch disk, 720 Kb COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: 33.229
REFINENCATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-56-3100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-56-3100
TELEPHONE: 215-56-3100
TELEPHONE: 115-56-3100
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REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide US-08-141-892A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-OCT-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-141-892A-23
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STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pomsylvania
COUNTRY: USA
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Sequence 18, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%; Score 17; DB 2; Lv 100.0%; Pred. No. 3.3e-12; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                       COUNTY ON THE COUNTY OF THE COUNTY OF THE COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: Windows SOFTWARE: Wordberfect 6.1

CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/583,447A FILING DATE: 05-JAN 1996
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/141,892 FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTONNEY, AGENT INFORMATION: NAME: DELUCA, MARK REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1702
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3109
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Sequence 23, Application US/08583447A
Patent No. 5879556
GRENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
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Batent No. 596220

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

MUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5962220ris

STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUUMALT: CUUMALT: CUUMALT: CUUMALT: CUUMALT: CUUMALT: CUUMALT: CUMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MAPPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1589
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
ATTONEY/ABENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                     TJU-1589
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-467-920-18
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COUNTRY: USA
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XGY: linear
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TOPOLOGY: linear
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US-08-467-920-23
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TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
TUTLE OF EQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STRRET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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Patent No. 596220

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: And Methods of Using The Same
ITLE OF INVENTION: And Methods of Using The Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSE: Wo. 596222018

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania
                                                                                                                                                                                                                               COUNTEXT: USAN

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: Windows
SOFTWARE: WORDErfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUJ-1702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGRH. 17 amino acids
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MEDIUM TYPE: Floppy disk COMPUTER: IEM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPETECT 5.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920 FILING DATE:
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Best Local Similarity 100.4
Matches 17; Conservative
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US-08-467-920-18
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GENERAL INFORMATION:
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USE-08-639-90-18

Sequence 18, Application US/08635930

Patent No. 660037

TREE OF INVENTION: Compositions That Specifically Bind TO TITLE OF INVENTION: Concertal Cancer Calls And Methods Of Using TITLE OF INVENTION: The Same NUMBER OF SEQUENCES: 54

CONTRESPONDER ADDRESS: 54

CONTRESPONDER ADDRESS: 54

CONTRY: USA PERIOR PROPERS: 54

CONTRY: USA PERIOR PROPES: 54

CONTRY: USA PERIOR PROPES: 54

COMPUTER: READALE FORM: MINOWS 3.1

SOFTWARE: Pernaylwania

CONFUREY: WORD PROPES: 180 66.1

COMPUTER: THE PERCOMMENT: US/08/635,930

FILING DATE: 24-RR-1996

CLASSIFICATION WUMBER: US/08/635,930

FILING DATE: 25-RR-1994

CLASSIFICATION WUMBER: 08/141,892

FILING DATE: 13-SEP-1994

CLASSIFICATION WUMBER: 21-SEP-1994

CLASSIFICATION WUMBER: 21-SEP-1994

TELEBROWE CHARACTERISTICS: 11-SELECTION WUMBER: 21-SEP-1496

TELEBROWE CHARACTERISTICS: 11-SELECTION WUMBER: 21-SEP-1496

TELEBROWE CHARACTERISTICS: 11-SEP-1496

TELEBROWE CHARACTERISTICS: 11-
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                                                                                                                 0; Indels
                                                       Score 17; DB 2; L
; Pred. No. 3.3e-12;
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                                                                                                                 Mismatches
                                     94.4%; Scc...
100.0%; Pre
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                                                                                                                                                                         2 TFYCCELCCYPACAGCN 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NTFYCCELCCYPACAGC 17
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Best Local Similarity 100.
                                                                                                                 Conservative
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                                  Query Match
Best Local Similarity
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US-08-467-920-23
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US-08-635-930-23
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| TITLE OF INVENTION: Compositions that Specifically Bind To TITLE OF INVENTION: The Same Call Control of the Total Control of
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Worderfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3109
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
EQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: peptide
US-09-193-997-18
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Search completed: March 26, 2005, 17:27:26 Job time : 24.4286 secs

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RESULT 2
US-10-082-014-79
Sequence 79, Application US/10082014
Publication No. US2003018588A1
                                                                                                                                                                                                                                                                                                                                                                                       US-09-930-915A-289
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Sequence 3, Appl
Sequence 3, Appl
Sequence 289, App
Sequence 289, App
Sequence 289, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 18, Appl
Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 289, App
                                                         March 26, 2005, 17:25:02; Search time 58.1786 Seconds (without alignments) 102.440 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24,
Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-082-014-79

US-10-621-684-3

US-10-621-684-3

US-10-806-006-289

US-10-805-913-289

US-10-905-719-3

US-10-621-684-18

US-10-621-684-19

US-10-621-684-19

US-10-621-684-19

US-10-621-684-23

US-10-621-684-20
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                          1407402 segs, 331100923 residues
                                       protein search, using sw model
                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
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Match Length
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Perfect score:
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290 App

290 App

290 App

286 App

286 App

21, Appl

22, Appl

22, Appl

22, Appl

41, Appl

42, Appl

43, Appl

44, Appl

46, Appl

46, Appl

47, Appl

48, Appl

48, Appl

40, Appl

41, Appl

41, Appl

42, Appl

44, Appl

46, Appl

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48, Appl

48, Appl

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41, Appl

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46, Appl

47, Appl

48, Appl

48, Appl

49, Appl

40, Appl

40, Appl

40, Appl

40, Appl

40, Appl

41, Appl

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US-10-621-684-25
US-00-930-910-915A-290
US-10-902-01-910
US-10-902-01-910
US-10-805-910-290
US-10-805-913-290
US-10-805-913-290
US-10-805-913-290
US-10-805-913-290
US-10-805-913-290
US-10-621-684-21
US-10-621-684-21
US-10-621-684-22
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US-10-621-684-41
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US-10-621-684-41
US-10-621-684-41
US-10-621-684-41
US-10-621-684-40
US-10-621-684-14
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## ALIGNMENTS

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Sequence 289, Application US/0930915A
Publication No. US20030138769A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: INMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
TITLE OF INVENTION: STABILITY
FILE REFERENCE: 4564/83101 ICC-102.2 PCT
CURRENT APPLICATION NUMBER: 60/295,867
FILE REFERENCE: 2001-08-15
PRIOR PLICATION NUMBER: 60/226,867
PRIOR PLICATION NUMBER: 60/225,843
PRIOR PLING DATE: 2000-08-16
PRIOR PLING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 313
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 289
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100.0%; Score 18; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0;
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ORGANISM: Escherichia coli
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100.0%; Score 18; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 15; 100.0%; Pred. No. 4.4e-13;
                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3109
                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684 FILING DATE: 17-7u1-2003 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 18; Conservative
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SEQ ID NO 289
LENGTH: 18
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US-10-806-006-289
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APPLICANT: Birkett, Ashley J.

TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED MITH AN N-TERMINAL CY
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patentin version 3.1
SEQ ID NO 79
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/10372076
; Sequence 80, Application US/20030198645A1
; Beulication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Priede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 80
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. U820040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                  4.4e-13;
                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 18; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 18; DB 14; Best Local Similarity 100.0%; Pred. No. 4.4e-13; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                  1 NTFYCCELCCYPACAGCN 18
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                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Escherichia coli
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US-10-372-076-80
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US-10-621-684-3
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1 NTFYCCELCCYPACAGCN 18

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1 NTFYCCELCCYPACAGCN 18

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CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                             APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Mahajan-Miklos, Shalina
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US/10/796,719
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US 60/443,098
PRIOR APPLICATION NUMBER: US 60/411,288
PRIOR PILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-38
PRIOR FILING DATE: 2003-01-10-12
NUMBER OF SEQ ID NOS: 149
SEC ID NOS: 149
SEC ID NOS: 149
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Publication No. US20040029182A1
GENERAL INPORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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100.0%; Pred. No. 4.4e-13;
atrive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
FILING DATE: 17-U1-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: OS-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                   Sequence 3, Application US/10796719
Publication No. US20050020811A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTFYCCELCCYPACAGCN 18
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Best Local Similarity 100.0
Matches 18, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-621-684-18
              US-10-796-719-3
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                                                                          SERBEAL INFORMATION: US.0040138863A1

APPLICANT: Page, Mark

APPLICANT: Priede, Mark

APPLICANT: Schmidt, Annette Elisabeth

APPLICANT: Schwidt, Annette Elisabeth

APPLICANT: Stober, Detlef

TITLE OF INVENTION: STABLIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR

TITLE OF INVENTION: GRECOLI HEPATITIS

FILE REFERENCE: 4564/87179

CURRENT APPLICATION NUMBER: US/10/677,074

CURRENT FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: 10/372,076

PRIOR FILING DATE: 2002-02-21

PRIOR PLILING DATE: 2002-02-21

PRIOR PLILING DATE: 2002-02-22

NUMBER OF SEQ ID NOS: 308

SSOTIME PRIOR PLING DATE: 2002-02-22

NUMBER OF SEQ ID NOS: 308

SSOTIME NOR SEQ ID NOS: 308

LENGTH: 18
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; Publication No. US20040156864A1
; General Information:
APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: TEMBLEITY
; FILE OF INVENTION: TEMBLEITY
; FILE OF INVENTION: TEMBLEITY
; FILE OF INVENTION: STABLLITY
; FILE OF INVENTION OF STABLLITY
; FILE OF INVENTION DATE: 1004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR APPLICATION NUMBER: 60/226,843
; RADOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SEQ ID NO 289
; LENGTH: 18
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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0;
US-10-677-074-80
; Sequence 80, Application US/10677074
; Publication No. US20040156863A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NTFYCCELCCYPACAGCN 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Escherichia coli
US-10-677-074-80
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US-10-805-913-289
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CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methode of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1xis
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                   Sequence 19, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 16;
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Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/583,447A FILING DATE: 05-JAN-1996 APPLICATION NUMBER: US 08/141,892 FILING DATE: 26-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-0ul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-568-3439
  1 TFYCCELCCYPACAGCN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TFYCCELCCYPACAGC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                   US-10-621-684-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-621-684-19
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US-10-621-684-24
                                                                                             RESULT 11
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CORRESPONDENCE ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
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                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                              94.4%; Score 17; DB 15; I 100.0%; Pred. No. 5.4e-12; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: TJU-1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-621-684-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: incar

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-621-684-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows SOFTWARE: WordPerfect 6.1
                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                       TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17 amino acids
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Philadelphia
                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: WoodGoost Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Pehladelphia
STATE: Pennsylvania
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/10621684
| Publication No. US20040029182A1
| GENERAL INFORMATION:
| APPLICANT: Waldman, Scott A.
| TILLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
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                                                                                                                                                                                                                                                                                                                 Score 15; DB 15; I Pred. No. 7.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                           | INFORMATION FOR SEQ 125-568-3100
| INFORMATION FOR SEQ 1D NO: 20:
| SEQUENCE CHARACTERISTICS:
| TOPOLOGY: 1 amino acids
| TOPOLOGY: 1 inear
| MOLECULE TYPE: amino acids
| MOLECULE TYPE: peptide
| SEQUENCE DESCRIPTION: SEQ ID NO: 20:
| US-10-621-684-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/583,447A FILING DATE: 05-JAN-1996 APPLICATION NUMBER: US 08/141,892 FILING DATE: 26-OCT-1993
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-621-684-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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100.0%; Pre
                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELBFAX: 215-568-3439 INFORMATION FOR SEQ ID NO: 25:
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 15; Conservat
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Best Local Similarity
Matches 15; Consert
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
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GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%; Score 16; DB 15; Length 16
100.0%; Pred. No. 6.5e-11;
Live 0; Mismatches 0; Indels
                                                                                                                                                                         PRIOR DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/583,447A
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFRWATION:
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APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                         NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU1-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-319
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10621684 Publication No. US20040029182A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 FYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FYCCELCCYPACAGCN 16
                               ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-621-684-24
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US-09-930-915A-290
i Sequence 290, Application US/09930915A
j Publication No. US20030138769A1
j GENERAL INFORMATION:
j APPLICANT: Birkett, Ashley J.
j TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
j TITLE OF INVENTION: STABLLITY
j FILE REFERENCE: 4564(83501 ICC-102.2 PCT
j CURRENT FILING DATE: 2010-08-15
pRIOR FILING DATE: 2000-08-15
pRIOR PRICKETING DATE: 2000-08-22
pRIOR APPLICATION NUMBER: 60/225,843
pRIOR PLING DATE: 2000-08-22
pRIOR PLING DATE: 2000-08-22
pRIOR PLING DATE: 2000-08-22
pRIOR PLING DATE: 2000-08-16
pRIOR PLING
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83.3%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels
4 YCCELCCYPACAGCN 18
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1 YCCELCCYPACAGCN 15
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US-09-930-915A-290
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Search completed: March 26, 2005, 17:44:31 Job time : 59.1786 sec8

4 YCCELCCYPACAGCN 18

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 26, 2005, 17:10:31 ; Search time 18.6429 Seconds (without alignments) 92.899 Million cell updates/sec

NTFYCCELCCYPACAGCN 18 US-10-775-481A-3 Title: Perfect score:

Scoring table: Sequence:

<u>©biGo</u> Gapop 60.0 , Gapext 60.0

283416 segs, 96216763 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heat-stable entero	enterotoxin - Yers	heat-stable entero	probable lysis pro	ŭ	hypothetical prote	alanine-tRNA ligas		insulin-like growt	=	hypothetical prote	_		_	gene EHS-2 protein	hypothetical prote	₩.	hypothetical prote	protein	T-cell translocati	probable rRNA meth	conserved hypothet	conserved hypothet	C.					
SUMMARIES	QI	QHEC2	A60103	QHEC1	QHEC4	QHECIB	868705	S31652	825659	D85845	T15414	T29133	E71476	I48922	A49617	C39370	AF0925	H84631	A82531	AF1043	174319	B72476	A24255	T17300	S34815	A32795	E71464	A83103	F81726	S
	Length DB	18 1	18 2	72 1	72 1	72 1	53 2	66 2		90 2		~	924 2	2482 2	2483 1	72 2		75 2				111 2		•		w	187 2	4	224 2	78
de	Query	100.0	55.6	55.6	38.9	в.	33.3	ë.	ω.	ω.	Ξ.	•	•	33.3	33.3	27.8	27.8	•		۲.	7.	27.8	۲.	7	27.8	۲.	27.8	7.	27.8	7.
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	Result No.	1	7	m	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote	hypothetical prote hypothetical prote	competence protein probable uridine p	protein ZC123.3 [i	cob(1) alamin adeno	probable exported HKRFX protein - hu	competence protein hypothetical prote		hypothetical prote	SRG1-like protein
T20398 F70405	D85888 A91044	AG2988 AC0923	G87721 AG0814	B65021	ACU189 QQBEC2	A99295 T24402	E90179	D71246	T49224
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230	243 243	246 247	263	267	277	291 306	308	316	316
27.8	27.8 27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8
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30 31	33.2	34 35	36	8 6	4 0	4 4 1 2	43	44	45

## ALIGNMENTS

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C;Accession: A01823
R;Chan, S.K.; Giannella, R.A.
R;Chan, S.K.; Giannella, R.A.
A;Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat A;Reference number: A01823; MUID:81264141; PMID:7021541
                                                                                                                                                                                                                                                                                                      A.M.Coeule type: protein
A.Residues: 1-18 - CHA>
A.Residues: 1-18 - CHA>
A.Cross-references: UNTROT:P01560
A.Experimental source: strain 18D, serotype 0.42:k86:H37
C.Comment: This enterotoxin is one of several, of differing molecular sizes, produced by idues of the heat-stable enterotoxin ST-I.
C.Superfamily: heat-stable enterotoxin ST-I.
C.Superfamily: heat-stable enterotoxin ST-I.
C.Keywords: enterotoxin; heat-stable protein
F;1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F;5-10,6-14,9-17/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                C,Species: Bscherichia coli
C,Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
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nilarity 100.0%; Pred. No. 2.7e-15;
Conservative 0; Mismatches 0;
heat-stable enterotoxin ST-2 - Escherichia coli
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Best Local Similarity
Matches 18; Conserv
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1 NTFYCCELCCYPACAGCN 18 1 NTFYCCELCCYPACAGCN 18 셤 ઠે

RESULT 2

Riguarino, A.; Giannella, R.; Thompson, M.R. Infect. Immun. 57, 649-652, 1989 AyTitle: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identica A;Reference number: A60103; WUID:89108617; PMID:2912902 A;Accession: A60103 heat-stable enterotoxin ST-Ia - Citrobacter freundii C;Species: Citrobacter freundii C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004 C; Accession: A60103

A,Molecule type: protein A,Residues: 1-18 «GUA» A,Cross-references: UNIPROT:Q7M0U3 C,Superfamily: heat-stable enterotoxin ST

Length 18; 0; Indels Query Match 55.6%; Score 10; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 10; Conservative 0; Mismatches 0;

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Gaps

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1 NTFYCCELCC 10

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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0373; A35978
R;Stieglitz, H:; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Fplasmid 20, 42-53, 1988
A;Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheric A;Reference number: JT0373; MUID:89202548; PMID:3071819
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P07965; GB:J03311; NID:g147875; PIDN:AAA24652.1; PID:g147876 R;Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
A;Tile: Isolation and nucleotide sequence determination of a gene encoding a heat-stable A;Reference number: A35978; MUID:90273381; PMID:2190361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat-stable enterotoxin ST-1b precursor - Escherichia coli
NyAlternate names: heat-stable enterotoxin ST-A2
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 30-Uun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: JS0292; A33068; Ā33067; A30567
R;Moseley, S.L.; Hardy, J.W.; Hug, M.I.; Echeverria, P.; Falkow, /S.
Infect. Immun. 39, 1167-1174, 1983
A;Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A;Reference number: JS0292; MUID: 83184648; PMID: 6341230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AjMolecule type: DNA
AjResidues: 1-72 <MOS>
AjCross-references: UNIPROT: 047185; UNIPROT: P07965; GB: M34916; NID: 9146407; PIDN: AAA2399C;
Rjowarakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, I. 219-226, 1989
AjTitle: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escheric AjReference number: A33068; MUID: 90034194; PMID: 2680769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A33068
A;Molecule type: DNA
A;Residues: 1-18,'A',20-72 < DWA>
A;Residues: 1-18,'A',20-72 < DWA>
A;Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A;Cross-references: GB:M292555; NID:g148029; PIDN:AAA24686.1; PID:g148030
A;Cross-references: GB:M292555; NID:g148029; PIDN:AAA24686.1; PID:g148030
A;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
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B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
B;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
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B;Note: the authors translated the codon AAG for residue 34
B;Note: the authors translated the codon AAG for residue 4
B;Note: the author
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, Residues: 54-72 <AIM>
, Guzman-Verduzco, L.M.; Kupersztoch, Y.M.
nfect. Immun. 57, 645-648, 1989
. Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
, Reference number: A30567; MUID:89108616; PMID:2643580
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C;Keywords: enterotoxin; heat-stable protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-53/Domain: propeptide #status predicted <PRO>
F;54-72/Product: heat-etable enterotoxin #status predic
F;59-64,60-68,63-71/Disulfide bonds: #status predicted
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100.0%; Pred. No. 0.1
iive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A; Residues: 1-72 <STI>
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A; Residues: 1-72 <ZHO>
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C; Superfamily:
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C;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross-references: GB: MS8746; NID:g145860; PIDN: AAA62776.1; PID:g145861
A, Experimental source: strain 18D
R; Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
A; Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheria, R, Reference number: J70373; MUID:89202548; PMID:3071819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              icross-references: UNIPROT:P01559, GB:V00612, GB:V01831, NID:g43704, PIDN:CAA23883.1, Finazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S. an. U. Biochem. Cell Biol. 61, 287-295, 1983
an. J. Biochem. Cell Biol. 61, 287-295, 1983
fittle: Primary structure determination of Escherichia coli heat-stable enterotoxin of Reference number: A30985; MUID:83284515; PMID:6349752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;So, M.; McCarthy, B.J.
Proc. Natl, Acad. Sci. U.S.A. 77, 4011-4015, 1980
A.fitle: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stale
A;Reference number: A01822; MUID:81054703; PMID:6254008
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                                                                                                                                                                                                                                                                   heat-stable enterotoxin ST-I precursor - Escherichia coli
NyAlternate names: heat-stable enterotoxin estAl
C;Species: Escherichia coli
C;Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 09-Jul-2004
C;Accession: A01822; A30985; A36732; JT0374; I51932
R;So, M; McCarthy, B.J.
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-54/Domain: propeptide #status predicted <PRO>
F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
F;55-64,60-68,63-71/Disulfide bonds: #status predicted
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A;Title: The heat-stable toxin I gene from Escherichia coli 18D.
A;Reference number: A36732; MUID:90368614; PMID:2203756
A;Accession: A36732
A;Molecule type: DNA
A;Residues: 1-72 < DAL>
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100.0%; Pred. No. 3e-05;
tive 0; Mismatches 0; Indels
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A,Residues: 1-72 <STI>
R,Sekizaki, T.; Akashi, H.; Terakado, N.
Am. J. Vet. Res. 46, 909-912, 1985
A,Title: Nucleotide sequences of the genes
A,Reference number: IS1932; MUID:85249571;
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KResidues: 55-72 <LAZ2>
A;Experimental gource: strain Fl1
R;Dallas, W.S.
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A;Residues: 1-69,'P',71-72 <RES>
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Best Local Similarity 100...
Loca 10; Conservative
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1 NTFYCCELCC 10
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A; Residues: 1-72 <LAZ>
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Gaps

Query Match 38.9 Best Local Similarity 100. Matches 7; Conservative

4 YCCELCC 10 ||||||| 58 YCCELCC 64

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heat-stable enterotoxin yst precursor - Yersinia enterocolitica (5.8pecies: Yersinia enterocolitica (5.8pecies: Yersinia enterocolitica (5.8pecies: Yersinia enterocolitica (5.8pecies: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004 (5.8pcession: 825659; A41474; A23114; 865849 (7.8pcession: 825659; A41474; A23114; 865849 (7.8pc.) (7.9pc.) (7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P07593; EMBL:X65999; NID:g48611; PIDN:CAA46801.1; PID:g48612 R;Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R. Infect. Immun. 58, 2983-2988, 1990 Affitle: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-A;Reference number: A41474; MUID:90354067; PMID:2201642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1.47,'S',49-71 <DEL>
A;Residues: 1.47,'S',49-71 <DEL>
A;Cross-references: GB:U09235, NID:g487394; PIDN:AAA18472.1; PID:g487395
B;Takao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A. Eur. J. Biochem. 152, 199-206, 1985
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A;Reaidues: 54-71 cTAK>
R;Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Mol. Microbiol. 14, 905-915, 1994
A;Title: Regulation of the Yersinia enterocolitica enterotoxin Yst gene. Influence of gr A;Reference number: 865849; MUID:95231297; PMID:7715452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable lysis protein S of prophage CP-933V 23340 [imported] - Escherichia coli (strain C;Species: Escherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession 1858945 S. Accession: 1858945 S. Accession: Basset B. J. Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Miture 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference, number: A85480; MUID:21074935; PMID:11206551
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A,Residues: 1-90 <STO>
A,Cross-references: UNIPROT:Q8X4MB; GB:AE005174; NID:g12516391; PIDN:AAG57224.1; GSPDB:G
A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced A,Reference number: A23114; MUID:86004705; PMID:4043080
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F:20-41/Domain: propeptide #status predicted <PRO>
F:42-71/Product: heat-stable enterotoxin yst #status predicted
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100.0%; Pred. No. 2;
tive 0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-71 <IBR>
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S68705
hear-stable enterotoxin Y-STC - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: S68705
R;Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FBBS Lett. 362, 319-322, 1995
A;Reterence number: S68705; MUID:95246844; PMID:7729521
A;Recension: S68705
A;Molecule type: protein
A;Recession: S68705
A;Reperimental source: strain 86-11
C;Superfamily: heat-stable enterotoxin ST
C;Superfamily: heat-stable enterotoxin F;41-46,42-50,45-53/Disulfide bonds: #status predicted
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Cispectors: Yersinia Kristensenii
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate in: Sibate in: Stackebrandt, E.
Submitted to the EMBL Data Library, November 1992
A;Reference number: S31652
A;Rescious: Data Library, November 1992
A;Status: preliminary
A;Rescious: DAA
A;Rescious: 1-66 < IBR-A;Rescious: UNIPROT:P31518; EMBL:X69218; NID:g48617; PIDN:CAA49152.1; PID:g48618
C;Superfamily: heat-stable enterotoxin ST
A;Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
A;Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble. C;Genetics:
A;Genetics:
A;Gene
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100.0%; Pred. No. 0.13;
ive 0; Mismatches
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100.0%; Pred. No. 1.9;
iive 0; Mismatches
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33.3%; Score 6; DB 2 100.0%; Pred. No. 1.7 ive 0; Mismatches

Query Match 33.3 Best Local Similarity 100. Matches 6; Conservative

CCELCC 46 S CCELCC 10

ઠે 셤 enterotoxin - Yersinia kristensenii

Local Similarity 100. 1es 6; Conservative

Query Match Best Loca Matches 12 PACAGC 17

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99

PACAGC

61

DB 2;

33.3%; Score 6; 100.0%; Pred. No :ive 0; Mismat

Local Similarity 100. hes 6; Conservative

A;Gene: Z3340 Query Match Best Loca Matches

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C;Accession: T15414
R;Getsel, C.
submitted to the EMBL Data Library, April 1996
A;Bescription: The sequence of C. elegans cosmid C05E11.
A;Reference number: Z18347
A;Accession: T15414
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule rype: DNA

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Ristephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A.Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A, Reference number: A71570; MUID: 99000809; PMID: 9784136
A, Rocession: E71476
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-924 <ARN>
A, Residues: 1-924 <ARN>
A, Residues: GB: AER001346; GB: AER001273; NID: 93329203; PIDN: AAC68344.1; PID: 93329209:
A, Experimental Bource: Serotype D, Strain UW-3/Cx
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R.Ludwig, T.; Tenscher, K.; Remmler, J.; Hoflack, B.; Lobel, P.
Gene 142, 311-312, 1994
A.; Title: Cloning and sequencing of cDNAs encoding the full length mouse mannose 6-phosphs
A.; Reference number: 148922; MUID:94252588; PMID:8194771
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A;Cross-references: EMBL:U04710; NID:9451552; PIDN:AAA19568.1; PID:9451553
C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II rept: C;Reywords: growth factor receptor F;1895-1934/Domain: fibronectin type II repeat homology <2F1>
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C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C; Accession: A49617; B39538; Ā48700; A46439; I52815; I65739; A57529
R; Szebenyi, G; Rotwein, P. Genomics 19, 120-129; 1994
A; Title: The mouse insulin-like growth factor II/cation-independent mannose 6-phosphate A; Reference number: A49617; MUID: 94245146; PMID: 8188212
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A; Residues: 1-2483 < SZES-
A; Residues: 1-2483 < SZES-
A; Cross-references: UNIPROCT: Q07113; GB:L22143; NID:g431410; PIDN:AAA39320.1; PID:g431412
A; Cross-reference: UNIPROCT: Q07113; GB:L22143; NID:g431410; PIDN:AAA39320.1; PID:g431412
A; Szebenyi, G.; Rotwein, P.
J. Biol. Chem. 266, 5534-5539, 1991
A; Title: Differential regulation of mannose 6-phosphate receptors and their ligands durin A; Recession: B39538; MUD:91170218; PMID:1848553
A; Accession: B39538
A; Molecule type: DNA
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
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C,Superfamily: alanyl-tRNA ligase
C,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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100.0%; Pred. No. 19;
tive 0; Mismatches
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100.0%; Pred. No. 10;
tive 0; Mismatches
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nes 6; Conserv
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C; Accession: E71476
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C;Genetics:
A;Note: SCIF2.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-534 <CEI>
A;Cross-references: UNIPROT:P54145; EMBL:U53338; NID:g1255840; PID:g1255843; PIDN:AAA961
A;Experimental source: strain Bristol N2; clone C05811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alanine-tRNA ligase (EC 6.1.1.7) - Chlamydia trachomatis (serotype D, strain UW3/Cx) C,Species: Chlamydia trachomatis
C,Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2003
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C;Species: Streptomyces coelicolor
C;Dece: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29133
R;Parkhill, J; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein COSE11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15414
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A;Introns: 43/1; 151/1; 182/3; 229/3; 339/2; 394/3; 423/3; 490/1
C;Superfamily: ammonium transport protein amt1
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                                                                 Length 90;
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33.3%; Score 6; DB 2; 100.0%; Pred. No. 7.2; :ive 0; Mismatches

Best Local Similarity 100. Matches 6; Conservative

A;Gene: CESP:C05E11.4

307 ACAGCN 312

13 ACAGCN 18

8

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-862 <PAR>

A; Accession: T29133

R.Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, August 1998 A.Reference number: 217215

33.3%; Score 6; DB 2; 100.0%; Pred. No. 9.7; tive 0; Mismatches

Conservative

397 YPACAG 402

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RESULT 12

11 YPACAG 16

Query Match Best Local Similarity Matches 6; Conserv

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Search completed: March 26, 2005, 17:25:59 Job time : 18.6429 secs
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Matches 5; Conserv
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                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <BOE>
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                                                                                                                                                                                                                                  A; Accession: A48700
A; Accession: A48700
A; Molecule type: mRNA
A; Molecule type: mll9500; NID: 9407325; PIDN: AAA16037.1; PID: 9407326
R; Stoger, R; Kubicka, P.; Liu, C.G.; Kafri, T.; Razin, A.; Cedar, H.; Barlow, D.P.
A; Stoger, R; Molecule type: mll990; MUID: 93214996; PMID: 9462104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Ressidues: 1-44 <RES
A;Cross-references: GB:L06445; NID:g293379; PIDN:AAA37921.1; PID:g553942
A;Accession: 165739
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ressidues: 93-106 <RE2>
A;Ressidues: 93-106 <RE2>
A;Ressidues: 93-106 <RE2>
A;Across-references: GB:L06446; NID:g293381; PIDN:AAA37922.1; PID:g293382
B;Liu, Z.; Mittanck, D.W.; Kim, S.; Rotwein, P.
Mol. Endocrinol. 9, 1477-1487, 1995
A;Title: Control of inaulin-like growth factor-II/mannose 6-phosphate receptor gene transvence number: A57529; MUID:96130821; PMID:8584025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross-references: GB:L06445; NID:g293379; PIDN:AAA37921.1; PID:g553942
A;Note: sequence extracted from NCBI backbone (NCBIN:128531, NCBIP:128532)
A;Stoegar., R.; Kubicka, P.; Liu, C.
Cell 73, 1-11, 1993
A;Title: Maternal-specific methylation of the imprinted mouse Igf2r locus identifies the A;Reference number: I52815; MUID:93214982; PMID:8462093
       A;Residues: 435-488 <522>
A;Cross-references: GB:M58586
A;Cross-references: GB:M58586
J: Biol. Chem. 268, 22338-22346, 1993
A;Title: Mutational analysis of the cation-independent mannose 6-phosphate/insulin-like is important for intracellular targeting of lysosomal enzymes.
A;Reference number: A48700; MUID:94042980; PMID:8226743
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C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 15-Mar-2004
C;Accession: C39370
R;Boehm, T.; Foroni, L.; Kaneko, Y.; Perutz, M.F.; Rabbitts, T.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No.
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Residues: 435-488 <SZ2>
Cross-references: GB:M58586
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Residues: 1-44 <STO>
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Proc. Natl. Acad. Sci. U.S.A. 88, 4367-4371, 1991
A;Title: The rhombotin family of cysteine-rich LIM-domain oncogenes: distinct members ar A;Reference number: A39370; MUID:91239569; PMID:2034676
A;References: D39370
A;Rolecule type: DNA
A;Residues: 1-72 eBOE>
A;Residues: 1-7
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57 --LLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
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ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/07/903,029
FILING DATE: 19920623
CLARSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENNET, Dennis A.
REGISTRATION NUMBER: 07-21(872)A
FREISCRATION NUMBER: 07-21(872)A
TELECOMMUNICATION NUMBER: 07-21(872)A
TELECOMMUNICATION NUMBER: 07-21(872)A
TELECOMMUNICATION NUMBER: 07-21(872)A
TELECOMMUNICATION NUMBER: 07-21(872)A
TELEPAX: (314)694-5009
TELEPAX: (314)694-9009
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENNICH: INFORMATICICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%; Score 166.5; DB 2;
35.1%; Pred. No. 9.5e-13;
tive 15; Mismatches 32;
US-08-141-892A-32
US-08-563-447A-32
US-08-6457-920-32
US-08-6457-930-32
US-09-138-937-32
US-09-138-237A-32
US-08-141-892A-31
US-08-141-892A-31
US-08-141-892A-31
US-08-583-447A-31
US-08-583-447A-31
US-08-635-930-31
US-08-635-930-31
US-08-635-930-31
US-08-635-930-31
US-09-138-237A-31
US-09-138-237A-31
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07901029
Patent No. 5969097
GENERAL INFORMATION:
APPLICANT: Wiegand, Roger C.
APPLICANT: Currie, Mark C.
APPLICANT: Fok, Kam F.
TITLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, Monsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 amino acids
AMINO ACID
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Best Local Similarity 35.1*
Matches 40; Conservative
       MOLECULE TYPE: peptide
     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TO
US-07-903-029-5
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7766, Ap
6455, Ap
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2321, Ap
14225, A
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Sequence 3, A
Sequence 28,
Sequence 7766
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548
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-16435-9
                                                                                                                                                                                                                                                                                                                                           513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
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Match Length
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112.2
122.3
122.3
122.2
122.2
122.2
122.2
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166.5 163.5 135

Result

811 811 60 60 60 60 60 60 67 67 67 67 67

66.5 66.5 66

64 · 5 64 64 64 64

63.5 63.5

Beq.

Minimum DB Maximum DB

Database

Scoring table:

Perfect score:

Run on:

Sequence:

26 61

Gaps

27;

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ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFRENCE/DOCKET NUMBER: 07-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 115 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-903-029-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P. O. Bo
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 WAAL-----AGGVTVQDGNFSFSLESVKKLKDLQE-----PQXPRVGKLRNFAPIPG 61
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62 EPVVPILCSNPNFPEELKPLCKEPNAQEILQRLEEIAEDPGTCEICAYAACTGC 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-07-903-029-6

Sequence 6, Application US/07903029

Sequence 7, Application US/07903029

Patent No. 5969037

APPLICANT: Wiegand, Roger C.

APPLICANT: Currie, Mark C.

APPLICANT: Fok, Kam F.

TITLE OF INVENTION: Human Guanylin

NUMBER OF SEQUENCES: 6

CORRESPONDENCES: 6

CORR
                                                                                                                                                                                                             Sequence 4, Application US/07903029;
Sequence 4, Application US/07903029;
Patent No. 5963097
GENERAL INFORMATION:
APPLICANT: Wiegand, Roger C.
APPLICANT: Currie, Mark C.
TITLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis A. Bennett, Monsanto Co., A3SG;
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,029
FILING DATE: 19920623
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: Bennet, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 07-21(872)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-5402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314)694-9009
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 115 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-903-029-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      St. Louis
Missouri
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                                                                                                                                                             RESULT 2
US-07-903-029-4
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STATE:
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4 WLLSVICLIGALÁVLVEGÝTVQDGDLSFPLESVKQLKHLREVQEPTLMSHKKFALRLPKP 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.6%; Score 135; DB 2; Length 115;
Best Local Similarity 33.0%; Pred. No. 7.2e-09;
Matches 37; Conservative 12; Mismatches 51; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 --PDVCYNPALPLDLQPVCASQEAASTFKALRITATD--ECELCINVACTGC 106
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Sequence 2, Application US/08145940

Sequence 2, Application US/08145940

Patent No. 5489670

GENERAL INFORMATION:
APPLICANT: Kita, Toshihiro
APPLICANT: Smith, Christine E.
APPLICANT: Fok, Kam F.
TITLE OF INVENTION: Human Uroguanylin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION UNDER:

FILING DATE: 19920623

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: 07-21(872)A

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 6:

SEQUENCE (TRABACTERISTICS:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE (TRABACTERISTICS:

LENGTH: 115 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 7
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                                                                                                                                                                        Score 81; DB 1; Length 15; Pred. No. 0.002;
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Pred. No. 0.0022;
2; Mismatches 0; Indels
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08145940
Petent No. 5499670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kita, Toshihiro
APPLICANT: Smith, Christine E.
APPLICANT: Fok, Kam F.
ITILE OF INFORMION: Human Uroguanylin
NUMBER OF SEQUENCES: 2
CORRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60680
COMPUTER READABLE FORM:
MEDTING TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,940
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                      Query Match
14.8%; Score 81; DB
Best Local Similarity 85.7%; Pred. No. 0.00
Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE DOCKET NUMBER: 07-21(808)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-583-447A-56 
; Sequence 56, Application US/08583447A
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%;
85.7%;
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TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Best Local Similarity 85.7-
Then 12; Conservative
                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-145-940-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-145-940-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                               US-08-145-940-1
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| Sequence 55, Application US/08583447A |
| Sequence 55, Application US/08583447A |
| Sequence 55, Application US/08583447A |
| Patent No. 1990.
| Patent No. 1990.
| Patent No. 1990.
| APPLICANT: Waldman, Scott A. |
| TITLE OF INVENTION: ST Receptor Binding Compounds and TITLE OF INVENTION: Methods of Using the Same NUMBER OF SEQUENCES: 56 |
| CORRESPONDENCES: 56 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris |
| STREET: One Liberty Place, 46th Floor |
| CITY: Philadalphia |
| STREET: Pennsylvania |
| COUNTRY: USA |
| COUNTRY: COUNTRY: USA |
| COUNTRY: COUNTRY: USA |
| COUNTRY: COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 0.0022;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FORDEY GIBK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-1AN-1996
CLASSIFICATION NUMBER: US 08/141,892
FILING DATE: 26-1AN-1993
CLASSIFICATION WHORER: US 08/141,892
FILING DATE: 26-07-1993
CLASSIFICATION: 435
ATTORNEY AGENT THYORMATION:
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF THE STATEMENT OF THE STATEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DDCELCVNVACTGC 15
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Best Local Similarity 85.74
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103
COMPUTER:READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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CURRENT PILLON:

PILE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS

FILE REFERENCE: REG195-B-PC7-US

CURRENT APPLICATION NUMBER: US/09/077,955A

CURRENT APPLICATION NUMBER: US/09/077,955A

CURRENT PILLING DATE: 1998-09-10

EARLIER APPLICATION NUMBER: US/44,271

EARLIER FILLING DATE: 1996-05-10

SOFTWARE: PAPENTING DATE: 20,0

SOFTWARE: PAPENTING DATE: 1996-05-10

SOFTWARE: PAPENTING DATE: 1996-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 DPQQQKSGLLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATDECEL----
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12.7%; Score 69.5; DB 4; Length 1940;
Best Local Similarity 26.2%; Pred. No. 39;
Matches 21; Conservative 7; Mismatches 19; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08896933
; Sequence 29, Application US/08896933
; Patent No. 621351
; GENERAL INFORMATION:
    TITLE OF INVENTION: TUNOR KILLING EFFECTS OF ENTEROTOXINS,
    TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
    CURRENT APPLICATION NUMBER: 08/252,978
    EARLIER APPLICATION NUMBER: 08/252,978
    EARLIER FILING DATE: 1994-06-02
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 29
    LENGTH: 221
                                                                                                                                                                                                                                      DB 2; Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                      49 DPQQQKSGLLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATDECEL
                                                                                                                                                                                                                         Query Match
12.7%; Score 69.5; DB 2; Length 15
Best Local Similarity 26.2%; Pred. No. 39;
Matches 21; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-077-955-34; Sequence 34, Application US/09077955A; Patent No. 6413740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 RLLRQGPCGSRDPĆANVTČS 149
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FEATURE:
NAME/KEY: Rat Agrin
                                                                               ; LOCATION: 1...1940
; OTHER INFORMATION:
US-08-644-271-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus sp
US-09-077-955-34
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Pred. No. 0.0048;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 30, Application US/08644271 |
| Sequence 30, Application US/08644271 |
| Patent No. 5814478 |
| GENERAL INFORMATION: |
| APPLICANT: Valentuela, et al. |
| TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS |
| TITLE OF INVENTION: AND LIGANDS |
| NUMBER OF SEQUENCES: 32 |
| CORRESPONDENCE S: 32 |
| ADDRESSEE: Regeneron Pharmaceuticals, Inc. |
| STREET: 777 Old Saw Mill Road |
| CITY: Tarrytown |
| CITY: Tarrytown |
| CTARTE |
| CORTESPONDENCE |
| CORTESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: NA
COUNTRY: NA
ZIP: 10591
COMPUTER READMBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATURG SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWBER: US/08/644,271
FILING DATE: 11-MEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, RODERT JURGES ATTORNEY/AGENT INFORMATION:
NAME: CODERT, RODERT JURGES 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
TELECOMMUNICATION INFORMATION:
        FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 DECELCINVACTGC 106
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Best Local Similarity 85.7<sup>3</sup>
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-583-447A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
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Gaps

33;

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TYPE: PRT
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                                                                                                                                                                                                                                                                             -----LSHDLIYNVSGPNYDKLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 VLQSAQGVYIKYHGFQVQLESVKKINELEEKQMSDPQQQKSGLLPDVCYNPALPL--DLQ 72
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                         Query Match
12.5%; Score 68.5; DB 3; Length 221;
Best Local Similarity 24.5%; Pred. No. 2.7;
Matches 26; Conservative 16; Mismatches 29; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels 35;
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                                                                                                                                                                                                                                                                                                                              73 PVCASQEAASTFKALRTIATDE------CELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 PVCASQEAASTFKALRIATDE------CELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                    60 TELKNÓEMÁTLFK-----DKNVDIYGVEYYHLCYLCENAERSAC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TELKNOEMATLFK-----DKNVDIYGVEYYHLCYLCENAERSAC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
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TITLE OF INVENTION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT PELLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/08/896,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 1999-05-18

EARLIER PILING DATE: 1999-05-18

EARLIER PILING DATE: 1997-07-18

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

EARLIER APPLICATION NUMBER: 08/25,978

EARLIER APPLICATION NUMBER: 07/891,718

EARLIER APPLICATION NUMBER: 07/891,718

EARLIER FILING DATE: 1992-06-01

EARLIER FILING DATE: 1990-01-17

EARLIER FILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER APPLICATION NUMBER: 07/416,577

EARLIER APPLICATION NUMBER: 07/416,530

EARLIER APPLICATION NUMBER: 07/416,530

EARLIER PILING DATE: 1999-10-03

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PARSEQ for Windows Version 3.0

SEGO ID NO 29
                                                                                                                                                                                                                                                       14 LVKNLQNIYFLYEGDPVTHENVKSVDQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/09314235
Patent No. 6338845
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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US-09-708-008B-29
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14 LVKNLQNIYFLYEGDPVTHENVKSVDQL------LSHDLIYNVSGPNYDKLK 59
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                                                                                                                                                                                                                                                                                                                                    Indels 35;
                                                                                                                                                                                                                                                                                  Query Match
12.5%; Score 68.5; DB 4; Length 221;
Best Local Similarity 24.5%; Pred. No. 2.7;
Matches 26; Conservative 16; Mismatches 29; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 PVCASQEAASTFKALRIIATDE-----CELCINVACTGC 106
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ADDRESSEE: Charles H. Harris
STREBT: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-Sep-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 08/252,978
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                   ) ORGANISM: Streptococcus pyogenes US-09-708-008B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atty)
CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-144-776B-16
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OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                       APPLICANT: SANO, KOHICHIRO
APPLICANT: KUMAZAMA, YOSHIYUKI
APPLICANT: KUMAZAMA, YOSHIYUKI
APPLICANT: SEGURO, KATSUTA
APPLICANT: SEGURO, KATSUTA
APPLICANT: MOTOKI, MASAO
TITLE OF INVENTION: TRANSCLUTAMINASE ORIGINATED FROM
TITLE OF INVENTION: CRASSOSTREA GIGAS
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS: 150
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END FO COMPATIBLE
COMPUTER: END FO COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: 28-58-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: J8-58-1995
FILING DATE: 28-58-1995
FILING DATE: 28-58-1995
FILING DATE: 38-58-1995
FILING DATE: 38-58-1995
FILING DATE: 38-58-1995
APPLICATION NUMBER: JP 7/3876
FILING DATE: 13-58-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-760-0 PCT
TELEPHONE: 103-13-3000
              Sequence 1, Application US/08525654A Patent No. 5736356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                              ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 VLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDVCYNPALPL--DLQ 72
                                                                                                                            44 LVKNLQNIYFLYEGDPVTHENVKSVDQLRSH-------DLIYNVSGPNYDKLK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 LVKNLÓNIÝFLÝEGDPÝTHÉNVKSVDQLRSH-------DLIÝNVSGPNYDKLK 89
                                                                                              15 VLQSAQGVYIKYHGFQVQLESVKKINELEEKQMSDPQQQKSGLLPDVCYNPALPL--DLQ 72
                                               30; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 251;
  DB 3; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 PVCASQEAASTFKALRTIATDE------CELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 TELKNOEMATLFK------DKNVDIYGVEYYHLCYLCENAERSAC 128
                                                                                                                                                                                        73 PVCASQEAASTFKALRTIATDE------CELCINVACTGC 106
                                                                                                                                                                                                                                        90 TELKNÓEMATLFK-----DKNVDIYGVEYYHLCYLCENAERSAC 128
Query Match
12.3%; Score 67.5; DB
Best Local Similarity 23.6%; Pred. No. 4.3;
Matches 25; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: And Bavari
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: PLORPY disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/882,431B

FILING DATE: June 25, 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION UNDRER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.6%;
Matches 25; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: Peptide US-08-882-4318-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Amino Acid
STRANDEDNESS: Unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARYLAND
                                                                                                                                                                                                                                                                                                                                         US-08-882-431B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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17 QSAQGVYIKYHGFQVQLESVKKLNE-----LEEKQMSDPQQQKSGLLPDVCYNPALPLD
                                                                                                                                                                                                                                                                                    Query Match
12.2%; Score 67; DB 1; Length 770;
Best Local Similarity 23.7%; Pred. No. 22;
Matches 22; Conservative 19; Mismatches 38; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 LOPVCASOBAAST-FKALRTIATDECELCINVA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 26, 2005, 16:51:12
Job time : 31.7226 secs
                                                                                                                                                                                                                       Crassostrea gigas
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                         : 770 amino acids
amino acid
```

RESULT 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

March 26, 2005, 16:48:40; Search time 105.613 Seconds (without alignments) 332.314 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-775-481A-55 Perfect score:

548 1 MSGSQLWAAVLLLLVLQSAQ......LRTIATDECELCINVACTGC 106 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1407402 seqs, 331100923 residues Searched:

1407402 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB A

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

**Database**:

Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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14: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB ID	DB	ΩI	Description	•
		1				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1
	356			17	US-10-479-606-5	Sequence 5, Ap	ppli
~	252.5			17	US-10-479-606-6	Sequence 6, Ap	ppli
m	166.5			σ	US-09-981-353-61	Sequence 61, Ap	pp]
4	166.5		115	14	US-10-235-994-22	Sequence 22, A	Appl
S	166.5			14	US-10-262-473-12	Sequence 12, A	Appl
9	166.5			17	US-10-479-606-4	Sequence 4, Ap	ppli
7	120			14	US-10-262-473-14	Sequence 14, A	Appl
œ	120			14	US-10-262-473-16	Sequence 16, A	Appl
0	97.5			σ	US-09-925-299-1162	Sequence 1162,	Ap
10	97.5	17.8	87	10	US-09-925-299-1162	Sequence 1162, Ap	, Ap
11	84		16	14	US-10-107-814-20	Sequence 20, A	Appl
12	84		85	σ	US-09-925-299-1527	Sequence 1527,	Ap
13	84		85	10	US-09-925-299-1527	Seguence 1527,	, Ap

Sequence 1, Appli Sequence 56, Appli Sequence 2, Appli Sequence 141, Appl Sequence 141, Appl Sequence 11, Appl Sequence 152, Appl Sequence 15295, Sequence 17295, Sequence 17295, Sequence 18159, Sequence 791, Appl Sequence 791, Appl Sequence 791, Appl Sequence 183110, Sequence 1563, Appl Sequence 1563, Appl Sequence 1563, Appl Sequence 1563, Appl Sequence 275, Appl Sequence 275, Appl Sequence 275, Appl Sequence 275, Appl Sequence 276, Appl Sequence 276, Appl Sequence 277, Appl Sequence 27, Appl Sequence 26, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 16, Appl	Sequence 2371, Ap
US-10-107-814-1 US-10-197-954-141 US-10-197-954-141 US-10-62-684-56 US-10-76-085-141 US-10-62-1684-55 US-10-621-684-55 US-10-621-684-55 US-10-621-684-55 US-10-621-684-55 US-10-621-684-55 US-10-621-684-55 US-10-424-599-275208 US-10-424-599-275208 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-072-012-791 US-10-335-977-6075 US-10-335-977-6077 US-10-335-977-6077 US-10-335-977-6077 US-10-335-977-6077 US-10-002-784A-26 US-10-002-784A-26 US-10-002-784A-26 US-10-002-784A-26 US-10-002-784A-16 US-10-002-784A-16	US-10-389-566-2371
14407740404040404040404040404044440474047444444	15
01106 1106 1106 1107 1107 1107 1107 1107	1074
44444444444444444444444444444444444444	12.3
669 669 669 669 669 669 669 669 669 669	67.5
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# ALIGNMENTS

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Substitution of the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapiens
US-10-479-606-5
US-10-479-606-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : PRT
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61 2 SGSQLWAAVLLILVLQSAQGVXIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDV 0; Gaps 7 ò 셤

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62 67

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APPLICANT: Lepiey, Denise,
APPLICANT: Returnian, Meera,
APPLICANT: Rastelli, Luca,
APPLICANT: Reiger, Daniel,
APPLICANT: Reiger, Daniel,
APPLICANT: Spyrek, Kimberly,
APPLICANT: Shong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 WAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSG-----
Sequence 22, Application US/10235994

Fublication No. US2030101002A1

GENERAL INFORMATION:

APPLICANT: Bartha, Gabor

APPLICANT: Walker, Michael

TITLE OF INVENTION: METHODS FOR ANALYZING GENE EXPRESSION PATTERNS

FILE REFERENCE: ICTTP012

CURRENT APPLICATION NUMBER: US/10/235,994

CURRENT FILING DATE: 2002-09-04

PRIOR PELICATION NUMBER: US/10/003,608

PRIOR FILING DATE: 2001-11-01

PRIOR PELING DATE: 2001-11-01

PRIOR PELING DATE: 2001-11-01

SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2:

LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 --LLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 BPVVPILĆSNPNFPEELKPLČKEPNAQEILQRLEBIABDPGTĆEIČAYAAČTĠĆ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%; Score 166.5; DB 14; Length 115; 35.1%; Pred. No. 2.3e-11; tive 15; Mismatches 32; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: INDESTRUCT.
FILE REFERENCE: 21402-462B
CURRENT APPLICATION NUMBER: US/10/262,473
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 12
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10262473
Publication No. US20030199442A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John,
APPLICANT: Burgess, Catherine,
APPLICANT: Gorman, Linda,
APPLICANT: Gorman, Linda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 35.1
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-473-12
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-262-473-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-235-994-22
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            13 MLDILAQNTQSVYIQYEGFQVNLDSVKKLDKLLEQLRGFHHQMGD--QRDPSIL---CSD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEK-----QMSDPQQQKSGLLPDVCYN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 WAAL-----AGGVTVQDGNFSFSLESVKKLKDLQE-----PQEPRVGKLRNFAPIPG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 WAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 -- LLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 EPVVPILCSNPNPPEELKPLCKEPNAQEILQRLEBIAEDPGTCEICAYAACTGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 46.1%; Score 252.5; DB 17; Length 109; 1 Similarity 52.5%; Pred. No. 1.9e-21; 53; Conservative 18; Mismatches 19; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.4%; Score 166.5; DB 9; Length 115; Best Local Similarity 35.1%; Pred. No. 2.3e-11; Matches 40; Conservative 15; Mismatches 32; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1800311CD1
US-09-981-353-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 PALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61. Application US/09981353
Patent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 53; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: oppossum
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US-09-981-353-61
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APPLICANT: Ratelli, Luca,
APPLICANT: Spytek, Kimberly,
APPLICANTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 1402-462B
CURRENT APPLICATION NUMBER: 60/329,917
FRIOR APPLICATION NUMBER: 60/328,056
FRIOR APPLICATION NUMBER: 60/349,575
FRIOR FILING DATE: 2001-10-09
FRIOR PELING DATE: 2001-10-29
FRIOR FILING DATE: 2001-10-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 WAAVLLLLVLQSAQGVYIKYHGFQVQLE-SVKKLNELEEKQMSDPQQQKSGLLPDVCYNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NFPEELKPLCKEPNAQEILQRLEEIAEDPGTCEICAYAACTGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 ALPLDLOPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.9%; Score 120; DB 14;
33.0%; Pred. No. 5.5e-06;
tive 12; Mismatches 39;
   PRIOR APPLICATION NUMBER: 60/328, use
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2002-05-16
PRIOR PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PRIOR DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/10262473 Publication No. US20030199442A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess, Catherine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alsobrook, John,
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Lepley, Denise,
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                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-262-473-14
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Matches 34; Conserv
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Publication No. US20050032684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Savas, Yuksel
TITLE OF INVENTION: treatment of respiratory airway problems
TITLE OF INVENTION: treatment of respiratory airway problems
FILE REFERENCE: 03100192aa
CURRENT APPLICATION NUMBER: US/10/479,606
CURRENT APPLICATION NUMBER: DE10127119.0
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
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APPLICANT: Reiger, Daniel,
APPLICANT: Reiger, Daniel,
APPLICANT: Spytek, Kimberly,
APPLICANT: Spytek, Kimberly,
APPLICANT: Spytek, Kimberly,
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 2102-462B
CURRENT APPLICATION NUMBER: US/10/262,473
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
                                                                              4,
                                                                                                                                                                      7 WAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSG-----
                                                                              Gaps
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Query Match 30.4%; Score 166.5; DB 14; Length 115; Best Local Similarity 35.1%; Pred. No. 2.3e-11; Matches 40; Conservative 15; Mismatches 32; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 115;
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30.4%; Score 166.5; DB 17; Length
Best Local Similarity 35.1%; Pred. No. 2.3e-11;
Matches 40; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: rat or homo sapiens (guanylin)
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Publication No. US20030199442A1
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APPLICANT: Burgess, Catherine,
APPLICANT: Gorman, Linda,
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Lepley, Denise,
Patturajan, Meera,
Rastelli, Luca,
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US-10-262-473-14
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APPLICANT:
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RESULT 12
US-09-925-299-1527
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US-10-107-814-20
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US-09-925-299-1162
; Sequence 1162, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT PILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 1999-03-12
; RIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1162
                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPRENDED PAIOZ.

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.8%; Score 97.5; DB 9; Length 87; Best Local Similarity 29.1%; Pred. No. 0.0019; Matches 23; Conservative 13; Mismatches 28; Indels
63 NFPEELKPLCKEPNAQEILQRLEEIAEDPGTCEICAYAACTGC 105
                                                                                                                                               Sequence 1162, Application US/09925299; Patent No. US20020055627A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 ATDECELCINV---ACTGC 106
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                    RESULT 9
US-09-925-299-1162
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LOCATION: (60)
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                                                                                NAME/KEY: SITE
LOCATION: (61)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (70)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (80)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1162
LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: Quanylate cyclase receptor agonist peptide
NAME/KRY: DISULFID
COCATION: (4)...(12)
NAME/KRY: DISULFID
COCATION: (7)...(15)
US-10-107-214-20
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Patent No. US20020055627A1
CENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
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ORGANISM: Artificial Sequence
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Best Local Similarity 92.9<sup>3</sup>
Matches 13; Conservative
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Best Local Similarity
Matches 23; Conserva
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LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                 NAME/KEY: SITE
1 LOCATION: (83)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1527
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Xaa equals any of the naturally occurring L-amino acids EX: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR PILING DATE: 2000-03-08
PRIOR RILING DATE: 1009-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                15.3%; Score 84; DB 9; Length 85; larity 33.8%; Pred. No. 0.07; Conservative 10; Mismatches 35; Indels
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Publication No. US20030040617A9
GENERAL INFORMATION:
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hes 23; Conserv
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US-09-925-299-1527
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KBY: SITE
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THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR PILING DATE: 2000-03-06
PRIOR PLING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1527
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (47)
OTHER INFORMATION: Xaa equals any
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OTHER INFORMATION:
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OTHER INFORMATION:
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Score 81; DB 14; Length 16;
Pred. No. 0.018;
2; Mismatches 0; Indels.
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85.7%;
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Best Local Similarity 85.7'
Matches 12; Conservative
                                                Query Match
Best Local Similarity 85.7
Matches 12; Conservative
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ORGANISM: Homo Sapien
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US-10-107-814-1
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                           NAME/KEY: SITE
COCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                  LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; Publication No. US20030073628A1
; Publication No. US20030073628A1
; GENERAL INFORMATION:
   APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS
; CURRENT APPLICATION NUMBER: US/10/107,814
; CURRENT PILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens

SEQ ID NO 1 LENGTH: 16

NAME/KEY: DISULFID LOCATION: (4)..(12) NAME/KEY: DISULFID LOCATION: (7)..(15)

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APPLICANT: K"ster, Hubert
APPLICANT: Siddigi, Suhaib
APPLICANT: Siddigi, Suhaib
APPLICANT: Siddigi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Cappute Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
FILE REPERENCE: 24743-2305
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT APPLICATION NUMBER: 60/306,019
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-197-954-141

'Sequence 141, Application US/10197954
'Publication No. US20030119021A1
'GENERAL INFORMATION:
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5.1.6
Compugen Ltd.
version 5
GenCore (c) 1993
       Copyright
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protein search, using sw model OM protein

March 26, 2005, 16:37:49 ; Search time 22.438 Seconds (without alignments) 454.541 Million cell updates/sec Run on:

1 MSGSQLWAAVLLLLVLQSAQ......LRTIATDECELCINVACTGC 106 US-10-775-481A-55 548 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	uroguanylin precur	guanylin precursor	guanylin precursor		guanylin precursor	alkanal monooxygen	coatomer protein z	proteinase inhibit	heat-stable entero	response regulator	exotoxin type A pr	NADP-specific glut	c-fps proto oncode	agrin - rat	exotoxin type A pr	exotoxin type A pr	hypothetical prote	tetrahydropteroylt	probable 60K inner	probable inner mem	heat-stable entero	protein-tyrosine k	hypothetical prote	ecdysone-induced p	phospholipase C (E	hypothetical prote	lamina associated	protein-tyrosine k	microfibril-associ
SUMMARIES	D	JC4651	JC7620	A46279	JN0318	B46279	JQ0413	S52521	845677	QHECIB	A82249	S18786	E83912	150618	AGRT	S18783	S29659	AC3027	G98257	B64701	E71818	QHEC4	TVFVFP	T01906	B53225	A48001	B84678	161730	TVFVFS	A49313
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ۇ ئى مە	Match	65.0	30.6	30.4	•	24.5	13.5	13.3	13.2	12.9	12.9	12.7	12.7	12.7	12.7	12.5	12.5	12.5	12.5	12.5	12.5	12.4	12.4	12.3	12.2	12.2	12.1	12.1	12.1	12.0
	Score	356	167.5	166.5	135	134.5	74	73	72.5		70.5	69.5	69.5		69.5	68.5		68.5	68.5	68.5	68.5	99	68	67.5	67	67	66.5	o	66.5	99
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hypothetical prote hypothetical prote	hypothetical prote phosphonates trans	probable ATP-bindi probable ATP-bindi	hypothetical prote	conserved nypotnet leucine aminopepti	protein-tyrosine-p protein-tyrosine-p	hypothetical prote carbon-monoxide de	hypothetical prote	ATP-dependent RNA
T23277 T32901	G72501 E83708	E91185 C86032	S47791	D83167	S28391 T45160	F72251 H70832	T46091	871392
0 0	0 0	~ ~	N C	N 64	- 0	~ ~	~ -	7 77
406 1259	235	274	274	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	711	445	852	993
12.0	11.9	11.9	6.11	11.8	11.8	11.7	11.7	11.7
99	65	65	65	64.5	64.5 64.5	64 44	49	6 4
30	33 33	3.4 3.5	36	38	4 9 9	417	4 4 6 4	. 4 . 2

## ALIGNMENTS

	human
	•
	precursor
н	vlin
RESULT JC4651	uroquanylin

N'Alternate names: guanylyl cyclase activating peptide II

N'Alternate names: guanylyl cyclase activating peptide II

C;Species: Home sapiens (man)

C;Dacession: JC4651; 863702; 868052

R;Miyazato, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo,
Biochem. Biophys. Res. Commun. 219, 644-648, 1996

A;Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanyl

A;Reference number: JC4651; MUID:96193705; PMID:8605041

A; Molecule type: mRNA A; Residues: 1-112 < MIX> A; Residues: 1-112 < MIX> A; Cross-references: UNIPROT: Q16661; GB: U34279; NID: g1236798; PIDN: AAC50416.1; PID: g12367 A; Hill, O.; Cetin, Y.; Gieslak, A.; Maegert, H.J.; Forssmann, W.G. Biochim. Biophys. Acta 1253, 146-149, 1995 Biochim. Biophys. Acta 1253, 146-149, 1995 A; Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precur A; Reference number: S63702; MUID: 96106424; PMID: 8519795

A; Accession: S63702
A; Molecule type: mRNA
A; Experimental source: tissue colon
A; Experimental source: tissue colon
B; Experimental source: tissue colon
B; Experimental source: tissue colon
A; Experimental source: tissue colon
A; Experimental source: tissue colon
A; Experimental source: tissue colon
B; Experimental source: tissue colon
A; FERS Lett. 374, 34-38
A; Title: GCAP-II: isolation and characterization of the circulating form of human urogua
A; FERS Colon
B; Moleculating form of human urogua

A;Accession: S68052 A;Molecule type: protein A;Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES> C;Comment: This protein, a member of the guanylin peptide family, is an endogenous activ

C, Superfamily: guanylin

C;Kerwords: intestine F;1-26/Domain: signal sequence #status predicted <SIG> F;27-112/Product: uroguanylin #status predicted <MAT>

Gaps ö Length 112; 22; Indels ch 65.0%; Score 356; DB 2; 1 Similarity 65.7%; Pred. No. 9.8e-30; 69; Conservative 14; Mismatches 22; Query Match Best Local

ö 61 99

2 SGSQLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDV g ò

CYNPALPLDLOPVCASOBAASTFKALRTIATDECELCINVACTGC 106 62

8 셤 RESULT

guanylin precursor, long form - European eel

Best Local Similarity 41.9% Matches 44; Conservative

요 ò 셤

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A,Accession: $25489
A,Molecule type: mRNA
A,Residues: 101-115 <MAE>
A,Sesidues: 101-115 <MAE>
A,Cross-references: EMBL:X67669; NID:956343; PIDN:CAA47901.1; PID:956344
C,Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl of the same receptor.
C,Superfamily: guanylin
C,Superfamily: guanylin
E,1-21/Domain: signal sequence #status predicted <SIG>F;22-115/Product: guanylin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Date: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JN0318; A4345; A38184; S25489
R;Wiegand, R.C.; Kato, J.; Currie, M.G.
Biochem. Biophys. Res. Commun. 185, 812-817, 1992
A;Title: Rat guanylin cDNA: characterization of the precursor of an endogenous activator A;Reference number: JN0318; WUID:92328783; PMID:1378267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-115 <MIES.
A; Residues: 1-115 <MIES.
A; Residues: 1-115 <MIES.
A; Cross-references: UNIPROT: P28902; GB: M93005; NID: g204540; PIDN: AAA41300.1; PID: g204541
B; Schulz, S.; Chrisman, T.D.; Garbers, D.L.
A; Biol. Chem. 267, 16019-16021, 1992
A; Title: Cloning and expression of guanylin. Its existence in various mammalian tissues.
A; Reference number: A43345; MUID: 92355545; PMID: 1379587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-115 cSCH>
A; Residues: 1-115 cSCH>
A; Cross-references: GB:M95493; NID:g204542; PIDN:AAA41302.1; PID:g204543
A; Experimental source: intestine
A; Note: sequence extracted from NCBI backbone (NCBIN:110474, NCBIP:110476)
B; Currie, M.G.; Fok, K.F.; Kato, J.; Moore, R.J.; Hamra, F.K.; Duffin, K.L.; Smith, C.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 947-951, 1992
A; Title: Guanylin: an endogenous activator of intestinal guanylate cyclase.
A; Reference number: A38184; MUID:92141235; PMID:1346555
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                                                                                                                                                                                                                                                                                                                                                                         4 WILSVICLIGALAVIVEGVTVQDGDLSFPLESVKQLKHIREVQEPTIMSHKKFALRIPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 WAAVLLLLVLQSA----QGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLL----
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 --LLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 BPVVPILCSNPNFPEELKPLCKEPNAQEILQRLEEIAEDPGTCEICAYAACTGC 115
                                                                                                                                                                                                                                                                                                                            7 WAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSG----
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                                                                                                                                                                                      Length 115;
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                                                                                                                                                                                                                                                             Indels
C;Superfamily: guanylin
C;Keywords: hormone; intestine
F;1.21/panain: signal sequence #status predicted <SIG>
F;22-115/Product: guanylin #status experimental <MAT>
                                                                                                                                                                               30.4%; Score 166.5; DB 1
35.1%; Pred. No. 4.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%; Score 135; DB 1; ilarity 33.0%; Pred. No. 8.3e-07; Conservative 12; Mismatches 51
                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                               Query Match
Best Local Similarity 35.14
Matches 40; Conservative
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A;Residues: 101-115 <CUR>
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                                                                                                                       Cidentie, N.W.; Cutler, C.P.; Cramb, G.
R; Comrie, M.M.; Cutler, C.P.; Cramb, G.
R; Comrie, M.M.; Cutler, C.P.; Cramb, G.
Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
A; Reference number: JC7620; MUID:21139737; PMID:11243845
A; Rocession: JC7620; MUID:21139737; PMID:11243845
A; Rocession: JC7620
A; Molecule type: mRNA
A; Residues: 1-116 < CCOM-
A; Rocie ences: GB:AJ301673
C; Comment: This protein, a member of a family of heat-stable peptides, is a potent extra axis. This peptide signalling system plays a role in osmoregulation in euryhaline telec C; Superfamily: guanylin
C; Keywords: heat-stable protein; osmoregulation
F; 1-28 Domain: signal sequence #status predicted <SIG>F; 29-116 / Product: guanylin precursor, long form #status predicted <MAT>
F; 133-39/Region: homologous #status predicted
F; 69-114/Region: highly conserved #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandlin precursor [validated] - human C.Species: Homo sapiens (man) C.Species: Accession: A46279; S29228; S29807
R.de Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V. Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
A.Fitle: Precursor structure, expression, and tissue distribution of human guanylin. A.Reference number: A46279; MUID:93028409; PMID:1409606
A.Resion: A46279
A.Rolecule type: mRNA
A.Residues: 1-115 - ADIA
A.Rolecule type: mRNA
A.Resiquence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
R.Wiegand, R.C.; Kato, J.; Huang, M.D.; Fok, K.F.; Kachur, J.F.; Currie, M.G.
FEBS Lett. 311, 150-154, 1992
A.Fitle: Human guanylin: CDNA isolation, structure, and activity.
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A.Residues: 1-115 <WIE>
A.Crose-references: GB:M97496; NID:g183414; PIDN:AAA35915.1; PID:g183415
R.Kuhn, M.; Raida, M.; Adermann, K.; Schulz-Knappe, P.; Gerzer, R.; Heim, J.M.; Forssman
FBBS Lett. 318, 205-209, 1993
A.Title: The circulating bioactive form of human guanylin is a high molecular weight pep
A.Reference number: S29807; MUID:93178628; PMID:8095028
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A; Molecule type: protein
A; Residues: 22-68 «KUH»
A; Experimental Source: plasma
A; Note: amino-terminal sequencing of mature form and molecular weight of mature form by
C; Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                      C;Species: Anguilla anguilla (European eel)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||:|| || :|||:
AVVLILLAPCFLQESQGVWVMDGDLSPPLEAVKVLKHLLGANTMSTPHPPNLG-SHAVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AAVLLLLV---LQSAQGVYIKYHGFQVQLESVKKLNE-LEEKQMSDPQQQKSGLLPDVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 NPALPLDLQPVCASQEAASTFKALRTIAT -- DECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.6%; Score 167.5; DB 2;
41.9%; Pred. No. 3.6e-10;
iive 10; Mismatches 44;
```

GDB:136460; OMIM:139392

A; Map position: 1p35-1p34

A;Gene: GDB:GUCA2 A;Cross-references:

of the same receptor.

A; Accession: S29228

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A;Cross-references: GB:X08036; GB:M34564; GB:M38298; NID:g45589; PIDN:CAA30831.1; PID:g4 R;Illarionov, B.A.; Protopopova, M.V.; Karginov, V.A.; Mertvetsov, N.P.; Gitelson, J.I. Mucleic Acids Res. 16, 9855, 1988
A;Title: Nucleotide Sequence of part of Photobacterium leiognathi lux region.
A;Reference number: S01697; MUID:89041570; PMID:3186447
                                                                                                                                                                                                                                                A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-34 < KLL3.
A;Cross-references: EMBL:X08036; NID:g45589; PIDN:CAA30831.1; PID:g45591
C;Comment: This enzyme catalyzes the oxidation of long-chain fatty aldehydes to long-cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Modecule type: DNA
A, Residues: 1-189 < BAD>
A, Residues: 1-189 < BAD>
A, Cross-references: UNIPOT: P53600; EMBL: Z48483; NID: g683777; PIDN: CAA88376.1; PID: g6837
A, Experimental source: strain AB972
B, FABAL; J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa submitted to the EMBL Data Library, August 1995
A, Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
Mysesidues: 1-189 cHAL.
A;Cross-references: EMBL.U33335; NID:9965076; PIDN:AAB68095.1; PID:9965083; MIPS:YPL010w
R;Yamazaki, S.; Harashima, S.; Sakaguchi, M.; Mihara, K.
B.; Biochem: 121, 8-14, 1997
A;Title: Identification and functional characterization of yeast zeta-COP.
A;Rteference number: JC5152; MUID:97211186; PMID:9058184
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NiAlternate names: protein LPA7w; protein YP8132.03; protein YPL010w; zeta-COP
Cispecies: Saccharomyces cerevisiae
Cibate: 08-May-1995 #sequence revisian 21-Jul-1995 #text_change 09-Jul-2004
CiAccesion: 552521; S59683; JC5152
CiAccesion: 552521; Churcher, C.
Ribadocock, K.; Churcher, C.
Submitted to the EMBL Data Library, February 1995
A;Reference number: S52519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 LLLLDOMSKGRFNFGVVRGLYHKDFRVFGVTMEDSRSITEDFHKMIMD--GSKSGVLHTD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: luxA
C;Superfamily: alkanal monooxygenase [FMN-linked] (bacterial luciferase)
C;Keywords: flavoprotein; FMN; luminescence; monooxygenase; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLLLVLQS-----AQGVYIK-YHGFQVQLESVKKLNELEEKQMSDPQQQKSGLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 16L
C,Superfamily: Vesicle coat complex COPI, zeta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GKNIEFPDVNVYPEAYLDKIPTCMTAESAAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 73; DB 2
26.0%; Pred. No. 3.8;
ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 74; DB 31.9%; Pred. No. 5.8; tive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 -----PDVCYNPALPLDLQPVCASQEAAST 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:RET3; YZC1
A;Cross-references: SGD:S0005931; MIPS:YPL010w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSGSQLWAAVLLLLVLQSAQGVYIKYH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 31.9%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S59683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: S52521
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Best Local (
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Graceise; we memeaculus (house

Graceise; we memeaculus (house)

Gracession: A5543; B46279

Riccitaty, D; Koshba, J.L.; Cohen, M.B.

Riccitaty, D; Koshba, J.L.; Cohen, M.B.

Grannics 24, 583-587, 1994

A; Title: Genemaic sequence of the murine guanylin gene.

A; Reference number: A5543; MuID:95229161; PMID:7713512

A; Reference number: A5543; MuID:9529161; PMID:7713512

A; Residues: L-116 (SGI)

A; Reference number: A4579; MuID:93028409; PMID:1409606

A; Status: nucleic acid sequence not shown
A; Reterence number: A4579

A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)

A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)

A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: L-116 (SGI)
A; Status: nucleic acid sequence actracted from NCBI backbone (NCBIP:115379)
C; Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
C; Superfamily: guanylin
C; Superfamily: guanylin
C; Superfamily: signal sequence #status predicted (SGI)
F; 1-21/Domain: signal sequence #status predicted (SGI)
F; 22-116/Product: guanylin #status predicted (SGI)
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A; Residues: 1-354 <ILL)
A; Residues: 1-354 <ILL)
A; Residues: 1-354 <ILL)
A; Cross-references: UNIPPOT: P09140; GB: X08036; GB: M34564; GB: M38298; NID: g45589; PIDN: CR
A; Cross-references: UNIPPODODOVA, M.V.; Karginov, V.A.; Mertvetsov, N.P.; Gitelson, I.I.
Bioorg. Khim. 14, 412-415, 1988
A; Title: Nucleotide sequence of genes of the luciferase alpha and beta subunits from Phd
A; Reference number: S06369; MUID: 88251495; PMID: 3382442
A; Accession: S06369
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ACVLSVLCLLGALAVLVEGVTVQDGDLSFPLESVKKLKGLREVQEPRLVSHKKFAPRLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                              --PDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.5%; Score 134.5; DB 1; Length 116; Best Local Similarity 36.0%; Pred. No. 9.5e-07; Matches 41; Conservative 15; Mismatches 43; Indels 15.
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us-10-775-481a-55.rpr

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R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Nature 406, 477-483, 2001
Nature 406, 477-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isola N,Alternate names: scarlet fever toxin C;Species: Streptococcus pyogenes phage A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS251 isolate California; strain N isolate United Kingdom; strain MGAS496 isolate Germany C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1999 C;Accession: S18786; S18796; S18795; S18795; S18799
                                                                                                                                               A; Reference number: A30567; MUID:89108616; PMID:2643580
                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-18,'A', 20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
A;Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response regulator VC1050 [imported] - Vibrio cholerae (strain N16961 serogroup
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: AB2249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SQLWAAVLLLLV-----LQSAQGVYIKYHGFQV-----QLESVKKLNELEEK----QMS
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C;Keywords: enterotoxin; heat-stable protein
F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F;54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.5; DI
Pred. No. 2.5;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 70.5; I
larity 30.7%; Pred. No. 14;
Conservative 21; Mismatches
                                                                     A;Residues: 54-72 cAIM>
R;Guzman-Verduzco, L.M.; Kupersztoch, Y.M.
Infect. Immun. 57, 645-648, 1989
A;Title: Rectification of two Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.9%;
Best Local Similarity 32.8%;
Matches 19; Conservative (
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A;Map position: 1
C;Superfamily: res
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase inhibitor - signal crayfish
C;Species: Pacifastacus leniusculus (signal crayfish)
C;Species: Pacifastacus leniusculus (signal crayfish)
C;Species: 07-oct-1394 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $45677
R;Johansson, M.W.; Keyser, P.; Soederhaell, K.
Eur. J. Biochem. 223, 389-394, 1994
A;Title: Purification and cDNA cloning of a four-domain Kazal proteinase inhibitor from A;Reference number: $45677; MUID:94333126; PMID:8055907
A;Accession: $45677
A;Accession: $45677
A;Accession: $45677
A;Accession: $45677
A;Coss-references: UNIPROT:Q26057; EMBL:X79512; NID:g498784; PIDN:CAA56043.1; PID:g4987
C;Cycwyords: serine proteinase inhibitor
C;Cycwyords: serine proteinase inhibitor homology <kPl>F;21-166/Domain: Kazal proteinase inhibitor homology <kPl>F;121-170/Domain: Kazal proteinase inhibitor homology <kPl>F;121-170/Domain: Kazal proteinase inhibitor homology <kPl>F;174-221/Domain: Kazal proteinase inhibitor homology <kPl>F;174-221/Do
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Neat-stable enterotoxin ST-Ib precursor - Escherichia coli

Neat-stable enterotoxin ST-Ib precursor - Escherichia coli

NyAlternate names: heat-stable enterotoxin ST-A2

C;Species: Escherichia coli

C;Species: Bacherichia coli

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: 39, 1167-1174, 1983

N;Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterot

A;Residues: 1.72 cMOS

A;Accession: 39, 1057-1174, 1983

A;Residues: 1.72 cMOS

A;Cross-references: UNIPROT:047185; UNIPROT:07965; GB:M34916; NID:9146407; PIDN:AA2399

R;Dwarachanath, P; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha,

A;Residues: 1.72 cMOS

A;Accession: A33068; MUD:90034194; PMID:2680769

A;Accession: A33068 MUD:90034194; PMID:2680769

A;Reterence number: A33068; MUD:90034194; PMID:2680769

A;Reterence number: A33068; MUD:90034194; PMID:2680769

A;Rotose-references: GB:M3255; ND:9148029; PIDN:AA24686.1; PID:9148030

A;Rotose-references: GB:M3255; ND:9148029; PIDN:AA24686.1; PID:9148030

A;Rotose-references: GB:M3365; MUD:90034194; PMID:6759126

A;Attle: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigeni

A;Reference number: A33067; MUD:83105138; PMID:6759126

A;Accession: A33067
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MSSLSLYTVQAVLILDQQGERIYAKYYQPPHRSDEGHQLLFNSVKKQKEFEKQLYRKTHK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 WAAVLLLLVLQSAQ-----GVYIKYHGFQVQLE----SVKKLNELEEK
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                                                                                                                                                              42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 69.5; DB
32.6%; Pred. No. 22;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: gdhA
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 17; Mismatches
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27.8%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 GLLPDVCYNPALPLDLQPVCASQ----EAAST
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Best Local Similarity 32.6*
Matches 30; Conservative
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Matches 25; Conserv
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A; Residues: 1-458 <STO>
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R; Melson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Sch. 174. 1271-1274, 1991
A; Title: Characterization and clonal distribution of four alleles of the speA gene encod A; Accession: S18786
A; Accession: S18787
A; Accession: S1878
A; Acc
                   Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
. Exp. Med. 174, 1271-1274, 1991
.Title: Characterization and clonal distribution of four alleles of the speA gene encod
.Reference number: S18782; MUID:92044323; PMID:1940804
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A;Residues: 1-236 <NEO>
A;Crose-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A;Experimental source: strain MGA5480 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Residues: 1-216 <NES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELKNQEMATLFKDKNVDIYSVEYYHLCYLCENAERSAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 69.5; DB 2; 27.3%; Pred. No. 11;
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C; Keywords: exotoxin
F; 1-22/Domain: signal sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S18792
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A;Cross-references: UNIPROT: 09KB34; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB058
A;Experimental source: strain C-125
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**R;Huang, C.C.; Hammond, C.; Bishop, J.M.
J. Mol. Biol. 181, 175-186, 1985
**A;Title: Nucleotide sequence and topography of chicken c-fps. Genesis of a retroviral on A;Reference number: I50618; MUID:85160839; PMID:3879969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-824 <HUA>
A;Cross.references: UNIPROT:Q90778; EMBL:X02266; NID:g63203; PIDN:CAA26155.1; PID:g87104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: c-fps
A;Introns: 75/3; 133/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 442/3; 512/3; 553/3;
A;Introns: 75/3; 133/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 42/3; 512/3; 553/3;
C;Reywords: ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                      -- PQ---- QQKS
                                                                                                                                                                                                                                                                  25;
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                                                                                                                                                                                                       Length 458;
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                                                                                                                                                                                                                                                                                                                                 5 QLWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSD--
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us-10-775-481a-55.rpr

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Search completed: March 26, 2005, 16:49:40 Job time : 23.438 secs
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Best Local Simil
Matches 26; C
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                                                                                                                                                                       Natice 6, 811-823, 1991

A/Itiles Structure and expression of a rat agrin.

A/Reference number: 190399, WID:9122570; PMID:1851019

A/Accession: JH0399, WID:9122570; PMID:1851019

A/Accession: JH0399 AWID:9122570; PMID:1851019

A/Accession: JH0399 AWID:9122570; PMID:1851019

A/Rederence number: 1-1779;1799-1599-1899 AWID: WID:9202798; PIDN:AAA40703.1; PID:9202804

A/Rederence number: MINREOR:225304, GB:W64780; NID:9202798; PIDN:AAA40703.1; PID:9202804

A/Rederence number: MARPED AWID: MAY: Percenson, K.; Francke, U.; Scholler, R.

A/Reference number: A38856; WID:92407628; PMID:1326608

A/Reference number: A38856; WID:92407628; PMID:3326608

A/Reference number: A38856; WID:92407628; PMID:332609

A/Reference number: A18856; WID:92407628; PMID:332609

A/Refere
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Fil28-1442/Domain: EGF homology <EG1>
Fil44-1445/Domain: EGF homology <EG2>
Fil44-1445/Domain: EGF homology <EG2>
Fil44-14476/Domain: EGF homology <EG3>
Fil48-1515/Domain: Bar homology <EG3>
Fil555-1706/Domain: Bar homology <EG4>
Fil555-1706/Domain: Bar homology <EG4>
Fil551-135/Domain: Bar homology <EG4>
Fil67-1959/Domain: Bar homology <EG4>
Fil67-1959/Domain: Bar homology <EG3>
Fil67-186,105-137,171-191,180-212,244-263,252-264,316-335,324-356,389-408,397-429,454-473
Fil476,1483-1494,1488-1504,1506-1515/Disulfide bonds: #status predicted
Fil45,672,827,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession. JH0399; A38856
C;Accession. JH0399; A38856
Neuron 6, 811-823, 1991
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
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26.2%; Pred. No. 1e+02;
7. Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 DPQQQKSGLLPDVCYNPALPLDLQPVCASQBAASTFKALRTIATDECEL
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F:869-992/Region: serine/threonine-rich
F:084-1086/Region: motor neuron attachment (L-R-E) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1147-1215/Region: serine/threonine-rich
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Best Local Similarity 26.2
Matches 21; Conservative
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RESULT 15 S18783

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NAtternate names: scarlet fever toxin
Cispecies: Streptococcus pyogenes phage
A;Variety: strain MGASISS isolate Nebraska; strain MGASISS isolate Yugoslavia; strain MGZICSPacies: 29-dan-1993 #sequence revision 29-dan-1993 #text_change 16-dul-1999
C;Accession: S18783; S18793; S18794; S18801; S18798
MSHSION: K, SCAILEVERT, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encodality.
- Streptococcus pyogenes phage (strain MGAS158 isola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-236 <NEL>
A; Residues: 1-236 <NEL>
A; Croses-references: EMBL:X61568; NID:g47289; PIDN:CAA43766.1; PID:g47290
A; Croses-references: Embl:X6158 isolate Nebraska unassigned phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18793
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note the nucleotide sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-236 <NEA>
A;Residues: 1-236 <NEA
A;Reperimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Retus: nucleic acid sequence not shown; translation not shown
A;Residues: 1-236 <NEZ>
A;Rocas-references: EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316
A;Reperimental source: strain MGAS491 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;A;Ceession: $18801
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Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
Experimental source: strain MGAS624 isolate Germany unassigned phage
Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A,Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A;Experimental source: strain MGAS495 isolate Germany unassigned phage
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 VLOSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSGLLPDVCYNPALPL--DLQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 LVKNLQNIYFLYBGDPVTHENVKSVDQL------LSHDLIYNVSGPNYDKLK 81
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F;1-22/Domain: signal sequence (fragment). #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
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ilarity 24.5%; Pred. No. 14;
Conservative 16; Mismatches
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                                               March 26, 2005, 16:37:18 ; Search time 91.2993 Seconds (without alignments) 594.533 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                   rattus
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      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                              1612378 seqs, 512079187 residues
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GUAU MOUSE
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COPZ_YEAST
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Q260<u>5</u>7
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
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Match Length
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Q9LUUO
HST2_ECOLI
Q8ZLBB
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Q9RC89
Q9KB34
Q8CM38
Q8E5L4
 Q72HT2
Q9KT55
Q949U6
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JUGUAL TA

JUGUAL RAT

DIANOV-1997 (Rel. 35, Last sequence update)

10.180V-1997 (Rel. 35, Last sequence update)

10.180V-1997 (Rel. 35, Last sequence update)

10.180V-1997 (Rel. 45, Rel. 48)

10.180V-1997 (Rel. 45, Rel. 48)

10.180V-1997 (Rel. 48)

10.180V-1991 (Rel. 48)

10.180V-1997 (Rel.
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Name=Guca2b
                              GUAU MOUSE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Notomys.

NCBL TaxID=184396;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469496; AAL77417.1; --
HSSP; Q16661; 1UYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
By similarity.
9FB5F88A9B1DD077 CRC64;
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ProDom; PD005588; Guanylin; 1.
SEQUENCE 107 AA; 11618 MW; 735110CACE60DA97 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0008047; F:enzyme activator activity; IEA. InterPro; IPR000879; Guanylin. Pfan; PF02058; Guanylin; 1. PRSF001849; Guanylin; 1.
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100.0%; Pred. No. 5e-48;
iive 0; Mismatches (
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Potential.
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                                                                              EMBL; U75186; AAB61209.1; -.
HSSP; Q16661; UVA.
RGD; 620044; Guca2b.
InterPro; IPRO00879; Guanylin.
Pfam; PP02058; Guanylin; 1.
PINSF; PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
ProDom; PD005588; Guanylin; 1.
                                                                                                                                                                                                                                                                                                                           Direct protein sequencing; Signal SIGNAL 1 21
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                        EMBL; U73898; AAB18331.1; -. EMBL; U41322; AAB18760.1; -. EMBL; U75186; AAB61209.1; -. HSSP; Q16661; 1UYA.
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1es 106; Conservative
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RESULT 3

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W REVISION TO 17.

WA Sanford L.P., Cohen M.B.;
Sanford L.P., Cohen M.B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

Stimulates this enzyme through the same receptor binding region as stimulates this enzyme through the same receptor binding region as the heat-stable enterotoxins. May be a potent physiological the heat-stable enterotoxins. May be a potent physiological regulator of intestinal fluid and electrolyte transport. May be an cortansport (By similarity).

C. autocrine/paracrine regulator of intestinal salt and water transport (By similarity).

C. -- SUBCELLULAR LOCATION: Secreted.

C. -- TISSUE SPECIFICITY: Localized predominantly in intestinal villical and the corticomedulary junction of the kidney.

C. -- SIMILARITY: Belongs to the guanylin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibc.ch).
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                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97434109; PubMed=9287995;
Whitaker T.L., Witte D.P., Scott M.C., Cohen M.B.;
"Uroquanylin and guanylin: distinct but overlapping patterns of messenger RNA expression in mouse intestine.";
Gastroenterology 113:1000-1006(1997).
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                                                      01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VCYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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By similarity.
Q -> R (in Ref. 1; AAB53314).
30FFICCE9D293DA8 CRC64;
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Pred. No. 3.9e-43;
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90.6%; Pred. No. 3...
7; Mismatches
   106 AA
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MGD; MG1:1270851; Guca2b.
InterPro: IPR000879; Guanylin.
Pfam; PF02058; Guanylin; 1.
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STANDARD;
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Best Local Similarity
Local 96; Conserve
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINE-EVBN/N; TISSUE-Kidney;

XX STRAINE-EVBN/N; TISSUE-Kidney;

XX STRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Staubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Banchow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

NA Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raheting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Uroquanylin (Guca2b protein) (Wns musculus adult male kidney cDNA, RIKEN full-length enriched library, clone: 6610009803 product:guanylate cyclase activator 2b (retina), full insert sequence).
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Kidney;
MBDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayaehlzaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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                                             106 AA
                                             PRT;
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STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miyazato M.;
Submitted (AUG-1996)
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                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukuda S., Fukunishi Y., Furuno M.,
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A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; BC004373; AAH24373.1; --
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STRAIN=C57BL/6J; TISSUE=Kidney;
X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nishi K., Kitsunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegaimai T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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                                    MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Muramateu M., Hayashizaki Y.; Winamalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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RGO; GO:0005615; G:extracellular space; TAS.

RGO; GO:0005182; P:cGMP biosgynthesis; IMP.

RGO; GO:0007589; P:fluid secretion; IMP.

RGO; GO:007589; P:negative regulation of blood pressure; InterPro; IPR000879; Guanylin.

PEAM; PP02089; Guanylin; 1.

PIRSF; PIRSF001849; Guanylin; 1.

PRINTS; PR00774; GUANYLIN.

PRINTS; PR00774; GUANYLIN.

PRODOM; PD005589; Guanylin; 1.

SEQUENCE 106 AA; 11627 MW; 30FPICCE9D293DA8 CRC64;
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STRAIN=C57BL/6J; TISSUE=Kidney;
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MGD; MGI:1270851; Guca2b.
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ID GUAU HUMAN
AC Q16661;
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-!- SIMILARITY: Belongs to the guanylin family.
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EMBL; Z50753; CAA9622.1; --
EMBL; Z50755; CAA94311.1; --
EMBL; U55058; AAC51729.1; --
PIR; UG4651, UG4651,
PDB; 1UYA; NMR; @=97-112.
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(Rel. 35, Last seq
(Rel. 45, Last ann
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MIM; 601271; -.
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112
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109
112 AA;
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les 69; Conserv
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P70107;
01-NOV-1997 (
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GUAU_CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96193705; PubMed=8605041; DOI=10.1006/bbrc.1996.0287; Miyazato M., Markazato M., Markazato M., Marebuo M., Marebuo H., Marebuo H., Marebuo H., Marebuo H., Marebuo M., Mangawa K., Marebuo H., Marebuo M., Marebuo M.,
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J. Pept. Res. 23.229-240(1998).
-!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It stimulates this enzyme through the same receptor binding region as the heat-stable enterotoxins. May be a potent physiological regulator of intestinal fluid and electrolyte transport. May be an autocrine/paracrine regulator of intestinal salt and water
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MEDLINE-98445220; PubMed-9774236;
Marx U.C., Klodt J., Meyer M., Gerlach H., Roesch P., Forssmann W.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "One peptide, two topologies: structure and interconversion dynamics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96649550; PubMed=7589507; DOI=10.1016/0014-5793(95)01075-P; Hess R., Kuhn M., Schulz-Knappe P., Raida M., Fuchs M., Klodt J., Adermann K., Kaever V., Cetin Y., Forssmann W.-G.; Holdtin T., Raever V., Cetin Y., Forssmann W.-G.; Holdtin and characterization of the circulating form of human uroguanylin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96106424; PubMed=8519795; DOI=10.1016/0167-4838(95)00204-4;
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94189775; PubMed=8141334;
Kita T., Smith C.E., Fok K.F., Duffin K.L., Moore W.M.,
Karabatose P.J., Kachur J.F., Hamra F.K., Pidhorodeckyj N.V.,
Forte L.R., Currie M.G.,
"Characterization of human uroguanylin: a member of the guanylin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hill O., Cetin Y., Cieslak A., Maegert H.-J., Forssmann W.-G., "A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): prevesor cDNA and colonic expression."; Biochim. Biophys. Acta 1253:146-149(1995).
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MEDLINE=97422613; PubMed=9268639; DOI=10.1006/geno.1997.4808;
Miyazato M., Nakazato M., Matsukura S., Kangawa K., Matsuo H.;
"Genomic structure and chromosomal localization of human
                                                                                                       activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maegert H.-J., Hill O., Forssmann W.-G.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                  01-NOV-1997 (Rel. 35, Last sequence update)
25-CGT-2004 (Rel. 45, Last annotation update)
27-CGT-2014 (Rel. 45, Last annotation update)
27-CGT-2014 (Guanylate cyclase activating peptide II) (GCAP-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 219:644-648(1996)
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SEQUENCE OF 89-112, AND DISULFIDE BONDS.
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SEQUENCE OF 97-112, AND DISULFIDE BONDS.
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      Created)
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01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
25-OCT-2004 (Rel. 45,
                                                                                                       Uroguanylin precursor
                                                                                                                                                                                                    (Human)
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                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                         Name=GUCA2B;
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SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Stomach and intestine.

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                                                                                                                                                                                                                                                                                                                                                                                                                         MIM, 601271; -.
GO, GO:0008048; F:calcium sensitive guanylate cyclase activat. . .; TAS.
GO; GO:0007588; P:excretion; TAS.
InterPro; IPR00879; Guanylin.
Pfam; PF02058; Guanylin; 1.
PIRSF; PF087049; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
PRODOM; PD005588; Guanylin; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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Kruhoeffer M., Meyer M.F., Schlatter E., Kaempf U., Cetin Y.,
Forssmann W.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CYNPALPLDLQPVCASQEAASTFKALRTIATDECELCINVACTGC 106
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65.7%; Pred. No. 2e-28;
ive 14; Mismatches 22; Indels
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Potential.
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SEQUENCE FROM N.A.
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Local s.
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=GUCA2B;
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It stimulates this enzyme through the same receptor binding region as the heat-stable entercoroxins. May be a potent physiological regulator of intestinal fluid and electrolyte transport. May be an autocrine/paracrine regulator of intestinal fluid and electrolyte transport.
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                                                                                                                                                                                                                                                                                                                                                                                                         14 AVVLILLIÓGTÓSVDÍKYOGYÓVÓLESVKKLKALEEGWVSSPRLÓAGDPOPAVCHHPALP
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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 autocrine/paracrine regulator of intestinal salt and water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Uroquanylin precursor (UGN) (Guanylate cyclase activator 2B)
(Guanylate cyclase C activating peptide II) (GCAP-II).
                                                                                                                                                                                                                                                                                                                                       Length 111;
                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                      By similarity.
By similarity.
7C3366A721FE0411 CRC64;
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SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                             69 LDLQPVCASQEAASTFKALRTIATDECELCINVACTGC
                                                                                                                                                                                                                                                                                                                                     Score 335; DB 1;
Pred. No. 2.8e-26;
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                                  SIMILARITY: Belongs to the guanylin family.
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                                                                                                                                                                                                                                                                   Uroguanylin.
                                                                                                                                                                                                                                            Potential.
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                      SUBCELLULAR LOCATION: Secreted
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InterPro; IRR000879; Guanylin.
Bfam; PP020268; Guanylin; 1.
PIRSP; PIRSPO1849; Guanylin; 1.
PRINTS; PRO0774; GUANYLIN.
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                                                                                                                                                                                                                                                                                                              12125 MW;
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97
67
100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQCKSGLLPDVCYNPALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 ALVFLVLLÓGTÓSVYIQÝQGPRVQLKSVKKLSDLEGQWAPSPRLQAQSPQPSVCHHSALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Uroguanylin: structure and activity of a second endogenous peptide that stimulates intestinal guanylate cyclase.";

Proc. Natl. Acad. Sci. U.S.A. 90:10464-10468(1993).

-!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. stimulates this enzyme through the same receptor binding region at the heat-stable enterotoxins. May be a potent physiological regulator of intestinal fluid and electrolyte transport. May be autocrine/paracrine regulator of intestinal salt and water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fan X., Hamra F.K., Freeman R.H., Eber S.L., Krause W.J., Lim R.W., Pace V.M., Currie M.G., Forte L.R., "Uroguanylin: cloning of preprouroguanylin cDNA, mRNA expression in the intestine and heart and isolation of uroguanylin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96193673; PubMed=8605009; DOI=10.1006/bbrc.1996.0255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Uroguanylin precursor (UGN) (Guanylate cyclase activator 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Didelphis marsupialis virginiana (North American opossum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . similarity.
8160573287BAB642 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 PDLÓPICQSEEAASIFQALRTIAGDDCELCVNVACTGC
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Biochem. Biophys. Res. Commun. 219:457-462(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.8%; Score 311; DB 1; 59.2%; Pred. No. 7.9e-24; iive 18; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uroguanylin.
By similarity.
By similarity.
By similarity.
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                                                          entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                         Potential
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                                                                                                                                                                                                      InterPro, IPR000879; Guanylin.
Pfam; PP002058; Guanylin; 1.
PIRSF; PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                               ProDom; PD005588; Guanylin; 1.
Signal. 1 27 Pc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12044 MW;
                                                                                                                                              EMBL; Z83746; CAB06042.1; -. HSSP; Q16661; 1UYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA;
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1 21 Po
22 94
95 109 Gu
98 106 By
101 109 By
109 AA; 11938 MW;
                                                                                                                                                              EMBL; Z73607; CAA97974.1; -. HSSP; Q02747; 1GNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=GUCA21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comrie M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
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PEPTIDE
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Matches
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Small and large intestine and atria and ventricles of heart. Both uroguanylin and prouroguanylin are found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides.";
Biochem. Biophys. Res. Commun. 259:141-148(1999).
-!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It stimulates this enzyme through the same receptor binding region as the heat-stable enterotoxins.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the guanylin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AVLLLLVLQSAQGVYIKYHGFQVQLESVKKINELEEKQMSDPQQQKSGLLPDV-CYNPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Jejunum;
MEDLINE=99268812; PubMed=10334930; DOI=10.1006/bbrc.1999.0719;
Maegert H.J., Hill O., Zucht H.D., Martin S., Meyer M.,
Forsamann W.-G., Adermann C.,
"Porcine guanylin and uroguanylin: cDNA sequences, deduced amino sequences, and biological activity of the chemically synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.8%; Score 278.5; DB 1; Length 109; 55.6%; Pred. No. 1.6e-20; ive 20; Mismatches 23; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y similarity.
AE948E210CA3AE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 PSDLOPVCENSQAANIFRALRSISQEDCELCINVACTGC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PLDLOPVCASOBAASTFKALRTIATDECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
2-OCT-2004 (Rel. 45, Last annotation update)
Guanylin precursor (Guanylate cyclase activator 2A)
Name=GUCA2A; Synonyms=GUCA2;
                                                                                                    -!- SIMILARITY: Belongs to the guanylin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uroguanylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct protein sequencing, Signal.
SIGNAL 1 23 Potential.
                 SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000879; Guanylin.
Pfam; PF02058; Guanylin; 1.
PRINSF; PIRSF00149; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
ProDom; PD005588; Guanylin; 1.
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65 78 Pot
98 106 By
101 109 By
109 AA; 12040 MW; A
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                                                                                                                                                                                                                                                                                                            EMBL; U49353; AAB00553.1; -. HSSP; Q16661; 1UYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LWAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQM-SDPQQQKSGLLPDVCYN 64
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIANE=21139737; PubMed=11243845; DOI=10.1006/bbrc.2001.4485; Comrie M.M., Cutler C.P., Cramb G.; "Cloning and Expression of Guanylin from the European eel (Anguilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thesis (2000), Department of School of Biology, University of Andrews, St Andrews, United Kingdom.

EMBL; AJ301672; CAC35448.1; --
HSSP; Q02747; 108R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 PKFPEELKPICOKPNAEELLERLETIAODPSTCEICAYAACAGC 109
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PIRSF, PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
PRODOM; PD005588; Guanylin; 1.
PROSITE; PS00197; ZFEZS FERREDOXIN; UNKNOWN 1.
SEQUENCE 108 AA; 11584 MW; 8A3B6D490E7CB58D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
6368BD1FB0B07A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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InterPro; IPR006058; 2Fe28 fd BS.
InterPro; IPR000879; Guanylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.8%; Score 174.5; DB 1
37.5%; Pred. No. 6.3e-10;
tive 16; Mismatches 38
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Pfam; PF02058; Guanylin, 1.
PIRSP; PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
ProDom; PD005588; Guanylin; 1.
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SEQUENCE FROM N.A. TISSUE=Placenta;
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                                                                                                                             Comrie M.M.
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ID GUAN HUMAN
Anguilla
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                 TISSUE-Intestine;

MEDLINE-22692502; PubMed=12684514; DOI=10.1074/jbc.M303111200;

Yuge S., Inoue K., Hydoo S., Takei Y.;

A novel guanylin family (guanylin, uroguanylin, and renoguanylin) in eels: possible osmoregulatory hormones in intestine and kidney.";

J. Biol. Chem. 278:2276-22733 (2003).

EMBL; AB080642; BAC76011.1; -.

HSSP; QO:0008047; F:enzyme activator activity; IEA.

InterPro; IPR006058; 2Fe2S fd BS.

InterPro; IPR000879; Guanylin.

PIRSF; PIRSF001849; Guanylin; 1.
                                                      8 AAVLLLLV---LQSAQGVYIKYHGFQVQLESVKKLNE-LEEKQMSDPQQQKSGLLPDVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AAVLLLLV---LQSAQGVYIKYHGFQVQLESVKKLNE-LEEKQMSDPQQQKSGLLPDVCY
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                   Anguilla japonica (Japanese eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anguilla anguilla (European freshwater eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                7;
         Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 108;
                                                                                                     64 NPALPLDLQPVCASQEAASTFKALRTIAT - DECELCINVACTGC 106
                                                                                                                  64 NPALPLDLQPVCASQEAASTFKALRTIAT -- DECELCINVACTGC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 30.6%; Score 167.5; DB 2; Length 1 Similarity 41.9%; Pred. No. 3.3e-09; 44; Conservative 10; Mismatches 44; Indels
                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIRSF; PIRSFULLY, GUANYLIN.
PRINTS; PR00774; GUANYLIN.
ProDom; PD005588; GUANYLIN. 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
                                                                                                                                                                                                        01-0TN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
          DB 2;
         30.6%; Score 167.5; DB 2
41.9%; Pred. No. 3.3e-09;
iive 10; Mismatches 44
                                                                                                                                                                                      108 AA.
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                                                                                                                                                                                    PRT;
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                                44; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                              Preprouroguanylin.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Name=uroguanylin;
                                                                                                                                                                                                                                                                                                        Anguilla.
NCBI_TaxID=7937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=GUCA211;
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Q98TH9
DD Q98TH
AC Q98TH
DT 01-JU
DT 01-JU
DT 01-JU
DT GUANA
DE GUANA
DE GUANA
OS AMBUÍ
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01-JUL-1993 (Rel. 26, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Guanylin precursor (Guanylate cyclase activator 2A) (Guanylate cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93011964; PubMed-1327879; DOI=10.1016/0014-5793(92)81387-2; Wiegand R.C., Kato J., Huang M.D., Fok K.F., Kachur J.F., Currie M.G.; "Human guanylin: cDNA isolation, structure, and activity."; FEBS Lett. 311:150-154(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AAVLLLLV---LOSAQGVYIKYHGFQVQLESVKKLNE-LEEKQMSDPQQQKSGLLPDVCY
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                                                                                            MEDLINE=21139737; PubMed=11243845; DOI=10.1006/bbrc.2001.4485; Comtien M.M., Cutler C.P., Cramb G.; "Cloning and Expression of Guanylin from the European eel (Anguilla anguilla).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Precursor structure, expression, and tissue distribution of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   Thesis (2000), Department of School of Biology, University of St.
L. Thesis (2000), Department of School of Biology, University of St.
R. Andrews, St. Andrews, United Kingdom.
R. EMBL, AJ301673; CAC35449.1; -.
R. PISSP, QC2747; 108R.
R. GO; GO:0008047; F:enzyme activator activity; IEA.
R. InterPro; IPR0006959; ZFe2S fd BS.
R. InterPro; IPR0008979; Guanylin.
R. PIRSP; PRESP; PRESPOSS8; Guanylin; 1.
R. PRESP; PRO0744; GUANYLIN.
R. PRODOM; PD005588; Guanylin; 1.
R. ProDom; PD005588; Guanylin; 1.
R. PRODOM; PD005588; Guanylin; 1.
R. PROSITE; PS00197; ZFE2S_FERREDOXIN; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 NPALPLDLQPVCASQEAASTFKALRTIAT--DECELCINVACTGC 106
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                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 281:1078-1085(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 30.6%; Score 167.5; DB 2 Local Similarity 41.9%; Pred. No. 3.5e-09; les 44; Conservative 10; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA
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MEDLINE=93028409; PubMed=1409606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Gap-I).
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=7936;
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12 VALALVTEAVQ---VEEGGFSFPLDAVKKLEELMGVDMTVKQSPRLAKTSTTA-VCTNPD 67
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Kruhoeffer M. Cetin Y., Kaempf U., Forssmann W.-G.;
Kruhoeffer M. Garly Co the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
stimulates this enzyme through the same receptor binding region as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Intestine;

MEDLINE=22692502; PubMed=12684514; DOI=10.1074/jbc.M303111200;
Yuge S., Inoue K., Hyodo S., Takei Y.;
A novel guanylin family (guanylin, uroguanylin, and renoguanylin) in eels: possible osmoregulatory hormones in intestine and kidney.";
J. Biol. Chem. 278:22726-22733 (2003).
EMBL; AB080641; BAC76010.1;
HSSP; Q02147; L08R.
GO; GO:008047; P:enzyme activator activity; IEA.
InterPro; IPR000879; Guanylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELBEKQMS---DPQQQKSGLLPDVCYNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                  62 EPVVPILCSNPNFPEELKPLCKEPNAQEILQRLEEIAEDPGTCEICAYAACTGC 115
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Skaryotei Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                          57 --LLPDVCYNPALPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 27.5%; Score 150.5; DB 2; Length 110; Local Similarity 39.2%; Pred. No. 1.8e-07; nes 40; Conservative 15; Mismatches 38; Indels 9;
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PIRSF: PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUANYLIN.
ProDom; PD005588 Guanylin; 1.
PROSITE; PS00197; 2FE25 FERREDOXIN; UNKNOWN 1.
SEQUENCE 110 AA; 11646 MW; B161A03A913894F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LPLDLQPVCASQEAASTFKALRTIA--TDECELCINVACTGC 106
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01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Guanylin precursor (Guanylate cyclase activator 2A).
Name=GUCA2A; Synonyms=GUCA2;
Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    Preprorenoguanylin.
Name-renoguanylin;
Anguilla japonica (Japanese eel).
                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7937;
                                                                                                                                                                                                                                                                                      Q7ZZS1;
01-JUN-2003
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P70664;
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GUAN CAVPO
                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                       Q7ZZS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochemistry 33:13581-13592(1994).
-!-FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
stimulates this enzyme through the same receptor binding region as
the heat-stable enterotoxins.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in ileum and colon. Found in
                                                                                                                                                                                                                                                                            Kuhn M., Raida M., Adermann K., Schulz-Knappe P., Gerzer R., Heim J.-M., Porssmann W.-G.;
"The circulating bloactive form of human guanylin is a high molecular weight peptide (10.3 kpa).";
FEBS Lett. 318:205-209(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 WAAVLLLLVLQSAQGVYIKYHGFQVQLESVKKLNELEEKQMSDPQQQKSG------
                       Hill O., Kuhn M., Zucht H.D., Cetin Y., Kulaksiz H., Adermann K., Klock G., Rechkemmer G., Forssmann W.-G., Magert H.J.; "Analysis of the human guanylin gene and the processing and cellular localization of the peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                        MEDLINE=93178628; PubMed=8095028; DOI=10.1016/0014-5793(93)80022-M;
                                                                                                                                                                                                                                                                                                                                                                                                                                              [5]
STRUCTURE BY NWR OF 101-115.
MEDLINE=95034794; PubMed=7947768;
Skelton N.J., Garcia K.C., Goeddel D.V., Quan C., Burnier J.P.;
"Determination of the solution structure of the peptide hormone guanylin: observation of a novel form of topological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0030250; F:guanylate cyclase activator activity; NAS.
GO; GO:003025179; F:bormone activity; NAS.
GO; GO:0007165; P:signal transduction; NAS.
InterPro; IPR000879; Guanylin.
Pfam; PR02058; Guanylin; 1.
PIRSF; PIRSF001849; Guanylin; 1.
PRINTS; PRSF00774; Guanylin; 1.
ProDom; PD005588; Guanylin; 1.
3D-structure; Direct protein sequencing; Signal.
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                                                                                                                          localization of the peptide.";
Proc. Natl. Acad. Sci. U.S.A. 92:2046-2050(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasma.
-!- SIMILARITY: Belongs to the guanylin family.
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Guanylin.
MEDLINE=95199289; PubMed=7892222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M97496; AAA35915.1; -.
EMBL; M95174; AAA58625.1; -.
EMBL; X74322; CAC22258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A46279; A46279.
PDB; IGNA; NMR; @=103-115.
PDB; IGNB; NMR; @=103-115.
PDB; 1O8R; NMR; A=22-115.
Genew; HGNC:4682; GUCAZA.
MIM; 139392; --
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SEQUENCE OF 22-68.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.2%; Score 149; DB 1; Length 107; ilarity 33.3%; Pred. No. 2.5e-07; Conservative 14; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                           Guanylin.
By similarity.
By similarity.
; C4BE4CE609409F45 CRC64;
the heat-stable enterotoxins.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the guanylin family.
                                                                                                                                                                                                                                                                                                                                                Potential.
                                                                                                                                                                                         EMBL; 274736; CAA98991.1; -.
EMBL; 274737; CAA98991.1; -.
HSSP; QO2747; IGNA.
InterPro; IPRO00879; Guanylin.
Pfam; PF02058; Guanylin; 1.
PIRSF; PIRSF001849; Guanylin; 1.
PRINTS; PR00774; GUNNYLIN.
ProDom; PD005588; Guanylin; 1.
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21 92 Gu
93 107 Gu
96 104 By
99 107 AA; 11483 MW; (
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Matches 34; Conserv
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DISULFID
SEQUENCE
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SIGNAL
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66 FPEELRPVCKEPNSQDILNRLAVIAQDPSTCEICAYAACAGC 107 Search completed: March 26, 2005, 16:48:35 Job time : 92.2993 secs g

67 LPLDLQPVCASQEAASTFKALRTIATD--ECELCINVACTGC 106

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March 26, 2005, 16:35:58; Search time 122.628 Seconds (without alignments)
353.241 Million cell updates/sec
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579
1 MGCRAASGLLPGVAVVLLLL.....RTIANDDCELCVNVACTGCL 112
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                                                      OM protein
                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                             Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:*

geneseqp2004s:*

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:*

Database

	Description	Aaw18498 Human GCA	Aaw10595 Guanylate	Abg74823 Human uro	Adr45875 Amino aci	Aaw18467 Human GCA	Aaw18478 Human GCA	Aaw23221 GCAP-II C	Aaw18484 Human GCA	Aaw23232 GCAP-II C	Aaw18485 Human GCA	Aaw23233 GCAP-II C	Aaw18486 Human GCA	Aaw23234 GCAP-II C	Aaw18468 Human GCA	Aaw18479 Human GCA	Aaw23222 GCAP-II C	Aaw18490 Human GCA	Aaw23237 GCAP-II C	Aaw18471 Human GCA	Aaw18480 Human GCA	Aaw23225 GCAP-II C	Aaw18472 Human GCA	Aaw18481 Human GCA	Aaw23226 GCAP-II C	Aaw18474 Human GCA
SUMMARIES	QI	AAW18498	AAW10595	ABG74823	ADR45875	AAW18467	AAW18478	AAW23221	AAW18484	AAW23232	AAW18485	AAW23233	AAW18486	AAW23234	AAW18468	AAW18479	AAW23222	AAW18490	AAW23237	AAW18471	AAW18480	AAW23225	AAW18472	AAW18481	AAW23226	AAW18474
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	Watch Length	112	112	112	112	108	108	108	84	84	81	81	78	78	77	77	77	73	73	70	70	70	69	69	69	67
	Match	100.0	100.0	100.0	100.0	95.7	95.7	95.7	76.9	76.9	74.1	74.1	71.2	71.2	70.3	70.3		67.2	67.2	64.8	64.8	64.8	63.9	63.9	ω.	62.5
	Score	579	579	579	579	554	554	554	445	445	429	429	412	412	407	407	407	389	389	375	375	375	370	370	370	362
1	No.	-	8	ო	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18		20		22		24	25

Aaw23228 GCAP-II C	Aaw18488 Human GCA	Aaw18491 Human GCA	Aaw23238 GCAP-II C	Adr45874 Amino aci	Aaw18492 Human GCA	Aaw23239 GCAP-II C	Aaw18469 Human GCA	Aaw23223 GCAP-II C	Abg74824 Opossum l	Aaw18489 Human GCA	Aaw23236 GCAP-II C	Aab53987 Human col	Aaw18475 Human GCA	Aaw23229 GCAP-II C	Aaw18493 Human GCA	Aaw23240 GCAP-II C	Adj18912 Human NOV	Aar62442 Guanylate	Aar69810 Expressio
2 AAW23228	2 AAW18488	2 AAW18491	2 AAW23238	8 ADR45874	2 AAW18492	2 AAW23239	2 AAW18469	2 AAW23223	6 ABG74824	2 AAW18489	2 AAW23236	3 AAB53987	2 AAW18475	2 AAW23229	2 AAW18493	2 AAW23240	7 ADJ18912	2 AAR62442	2 AAR69810
67	69	99	99	106	64	64	26	26	109	43	43	82	38	38	37	37	115	94	94
62.5	62.2	61.5	61.5	61.5	59.9	59.9	51.8	51.8	43.5	39.7	39.7	37.3	35.1	35.1	34.0	34.0	28.4	28.1	28.1
362	360	356	356	356	347	347	300	300	252	230	230	216	203	203	197	197	164.5	162.5	162.5
36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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## ALIGNMENTS

This sequence represents a precursor of the guanyl cyclase C activating peptide, GCAP-II, which affects insulin secretion by the beta cells in the pancreas. This peptide is useful for treating pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the gastrointestinal, respiratory and urogenital apparatus, disorders of the cardiovascular and nervous systems, disorders of the cardiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GCAP-II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP-II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP-II (89-112) and GCAP-II (89-113) and treatment of the above disorders e.g. gene therapy for diabetes fragments - have insulinotropic Kruhoeffer M, Meyer M, Pardigol A, Heine G; Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human. New guanyl cyclase C activating peptide fragactivity, useful for treating diabetes, etc. AAW18498 standard; protein; 112 AA. Human GCAP-II precursor protein. Example 6; Fig 11; 33pp; German. 95DE-01043628. 95DE-01043628. (first entry) Forssmann W, Kist A, WPI; 1997-290350/27. (FORS/) FORSSMANN W. N-PSDB; AAT65115. DE19543628-A1. Homo sapiens. 24-NOV-1995; 24-NOV-1995; 22-APR-1998 28-MAY-1997. AAW18498; RESULT 1 AAW18498 

intramuscular

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against GCAP-II are useful as immunoassay reagents. GCAP-II is administered at, e.g. 100-1200 microg/day by intravenous or intramuscula origidation or 300-1200 microg/day subcutaneously. It may also be given orally, intranasally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-II was chemically synthesised, or isolated by chromatography from transformed eukaryotic or prokaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II, generation of cGMP was increased in a dose dependent manner. GCAP-II influences cGMP production via known receptor for heat stable enterotoxin. Other stomach, intestinal, pancreatic and liver cells also responded to GCAP-II, e.g. via changes in intracellular Ca2+ ion concentration
                                                                                                                                                                                                                                      Sequence 112 AA;
                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; guanylate cyclase; activating peptide; GCAP-II; cGMP; transepithelial transport; treatment; kidney; intestinal; respiratory; urogenital; circulatory; nervous system, disorder; disease; endocrine; sensory; system; osteopoxosis; dental; pentess; diabetes; hypophysis; gastrointestinal tract; diarrhoea; gene therapy; probe; recombinant production; transgenic animal; antibody; immunoassay reagent.
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                                                                                                                                                                                1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ
                                                                                                                                           1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guanylate cyclase activating peptide II - increases cGMP formation, a controls transport of water and electrolytes across epithelial cells.
                                                                                                        Gaps
                                                                                                                                                                                                                      61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112
                                                                                                                                                                                                                                           ö
                                                                    Length 112;
                                                                                                        Indels
                                                                100.0%; Score 579; DB 2;
100.0%; Pred. No. 4.5e-57;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guanylate cyclase activating peptide II.
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/label= sig_peptide
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/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                         AAW10595 standard; protein; 112
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                                                                                            Best Local Similarity 100.
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FORS/) FORSSMANN W
                                                                                      Local Similarity
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                                   Sequence 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                               AAW10595;
                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                              Apical membrane; mucosal epithelial cell; respiratory tract; judnoshine triphophate; guanylate cyclase C; G protein-coupled receptor; guanoshine triphophate; cyclic guanoshine monophosphate; cyclic guanoshine monophosphate; cyclic chloride ion secretion; inhalation; membrane-associated type II protein kinase; mucus fluidisation; cystic fibrosis transmembrane conductance regulator; breathing disorder; mucus secretion; antiasthmatic; antinflammatory; bronchial asthma; chronic bronchitis; cystic fibrosis; uroguanylin; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel medicament in a formulation that is delivered to the apical membrane of mucosal epithelial cells through the respiratory tract. The medicament contains at least one peptide that activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor that catalyses conversion of guanosine triphophate to cyclic guanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for treating respiratory disease, comprises a peptide that activates guanylate cyclase C, and is delivered to the apical membrane through the respiratory tract.
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                                                                                                         9
                                                                                             1 MGCRAASGLIPGVAVVILLILQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ
                                                                        1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ
                                     Gaps
                                                                                                                                                112
                                                                                                                                                                        SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112
                                     ;
0
                                                                                                                                                61 SILPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL
100.0%; Score 579; DB 2; Length 112; 100.0%; Pred. No. 4.5e-57;
                                   Indels
                                       ö
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Human uroguanylin precursor SEQ ID 5.
                                                                                                                                                                                                                                                                                 ABG74823 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 3; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2002; 2002WO-DE002040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2001; 2001DE-01027119.
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                   Best Local Similarity 100.
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CETI/) CETIN Y. (SAVA/) SAVAS Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200298912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cetin Y,
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monophosphate (cGMP) and is present on the apical (air) side of respiratory epithelial cells but not on the basolateral (blood) side. CGMP activates membrane-associated type II protein kinase which in turn activates the regulatory domain of the cytic fibrosis transmembrane conductance regulator, resulting in secretion of chloride ions and water from the cells, causing fluidisation of the mucus. The products of the invention are used to make an inhalation device containing the medicament for diagnosing diseases that are accompanied by breathing disorders or disorders of mucus secretion in the respiratory tract, by detecting at least one GCC activator. The products of the invention have antiasthmatic and antiinflammatory activity. The method is useful for diagnosing and treating diseases accompanied by breathing disorders or disorders of the companied by breathing disorders or disorders of the companied by breathing disorders or disorders of improves fluidity and evacuation of bronchial mucus and acts locally chronic bronchitis and cystic fibrosis. The product of the invention improves fluidity and evacuation of bronchial mucus and acts locally cance the medicament does not enter the bloodstream), so systemic side effects are minimised. Only very small doses of the medicament are required. This sequence represents a precursor of the human guanylate the contraction of the contraction of the human guanylate the contraction of the medicament are contraction. the invention 888888888888888888888888888

Sequence 112 AA;

ö Gaps ö 100.0%; Score 579; DB 6; Length 112; 100.0%; Pred. No. 4.5e-57; 0; Indels 0; Mismatches Matches 112; Conservative Best Local Similarity Query Match

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61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112 SLLPAVCHHPALPQDLQPVCASQBASSIFKTLRTIANDDCELCVNVACTGCL 112

ADR45875 standard; peptide; 112 AA

ADR45875;

18-NOV-2004

Amino acid sequence of ST receptor ligand uroguanylin. (first entry)

heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer; oesophageal cancer; colorectal cell; gastric cell; oesophageal cell; uroguanylin.

Homo sapiens

WO2004071436-A2.

26-AUG-2004.

10-FEB-2004; 2004WO-US003765.

2003US-0446730P. 10-FEB-2003; (UYJE-) UNIV JEFFERSON THOMAS.

Wolfe HR; Schulz S, Park J, Waldman SA, Pitari GM,

WPI; 2004-615913/59.

Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell. 

activating peptide, GCAP-II, obtained by digestion with endoprocease Arg-C. GCAP-II is involved in insulin secretion by pancreatic beta cells.
This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the castionstestinal, respiratory and urogenited apparatus, disorders of the cardiovascular and nervous systems, disorders of the sense organs and diseases associated with GCAP II (89-112) deficiency.

New guanyl cyclase C activating peptide fragments - have insulinotropic activity, useful for treating diabetes, etc.

Peptides AAW18467-W18470 represent fragments of the guanyl cyclase C

Claim 3; Fig 3; 33pp; German.

Claim 6; SEQ ID NO 56; 97pp; English.

ö The specification describes a method for increasing the number of heat stable toxin (ST) receptor molecules on the surface of a metastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the number of ST receptor molecules on the surface of the cancer cell is increased. Therapeutic compositions comprising components which target ST receptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that hat have diseases that affect colorectal, gastric and oesophageal cells, including colorectal, gastric or oesophageal cancers. The present sequence represents a ST receptor ligand used in the method 8 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQYQGFRVQLESMKKLSDLRAQWAPSPRLQAQ 60 1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ Gaps ö Heine 61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112 Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human. ö Human GCAP-II (89-112) endoprotease Arg-C digested fragment 1. Query Match 100.0%; Score 579; DB 8; Length 112; Best Local Similarity 100.0%; Pred. No. 4.5e-57; Pardigol A, Indels ö Meyer M, 0; Mismatches of the invention, designated uroguanylin. Kruhoeffer M, Ź AAW18467 standard; peptide; 108 95DE-01043628. 95DE-01043628. 23-APR-1998 (first entry) Matches 112; Conservative Forssmann W, Kist A, (FORS/) FORSSMANN W. WPI; 1997-290350/27. Sequence 112 AA; DE19543628-A1 24-NOV-1995; 24-NOV-1995; Homo sapiens 28-MAY-1997. AAW18467; Query Match RESULT 5 AAW18467 8X33333333333333X8 셤 ð ઠ 셤

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Gaps

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Length 108; 0; Indels

2.8e-54; DB 2;

100.0%; Preq. .... Score 554;

Matches 108, Conservative

Similarity

Query Match Best Local

95.7%;

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1 AASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESWKKLSDLBAQWAPSPRLQAQSLLP

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5 AASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLP

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       reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP-II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP-II (89-115) cDNA are useful for diagnosis and treatment of the above disorders e.g. gene
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                                                                                                                                                                   9
                                                                                                                                                            1 AASGILPGVAVVLLILIQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLP
                                                                                                                                             5 AASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLP
This peptide can be used for treatment of electrolyte effects on bone
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                              Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human.
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                                                                                                                                                                                                      61 AVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 108
                                                                                                                                                                                          65 AVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 112
                                                                                                95.7%; Score 554; DB 2; Length 108; 100.0%; Pred. No. 2.8e-54; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Human GCAP-II (89-112) trypsin digested fragment 1.
                                                                                                                                                                                                                                                                        AAW18478 standard; peptide; 108 AA
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                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                Query Match
Best Local Similarity 100.
Matches 108; Conservative
                                                        therapy for diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FORS/) FORSSMANN W.
                                                                              Sequence 108 AA;
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Human; guanylate cyclase; activating peptide; GCAP-II; CGMP; transepithelial transport; treatment; kidney; intestinal; respiratory; urogenital; circulatory; nervous system; disorder; disease; endocrine; sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis; gastrointeetinal tract; diarrhoea; gene therapy; probe; recombinant production; transgenic animal; antibody; immunoassay reagent.

DE19528544-A1 Homo sapiens.

06-FEB-1997.

GCAP-II C-terminal fragment prepared by endoproteinase Arg-C.

(first entry)

29-OCT-1997

AAW23221;

AAW23221 standard; peptide; 108 AA.

AAW2322 RESULT

Guanylate cyclase activating peptide II - increases cGMP formation, an controls transport of water and electrolytes across epithelial cells. Claim 3; Page 4-5; 15pp; German. 

peptides AAW18478-W18483 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with trypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenital apparatus, disorders of the captiratory, readiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GGAP II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP-II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP II (89-113) conduction of GCAP-II (89-112) and drawn are useful for diagnosis and treatment of the above disorders e.g. gene

therapy for diabetes

Sequence 108 AA;

New guanyl cyclase C activating peptide fragments - have insulinotropic activity, useful for treating diabetes, etc.

Claim 3; Fig 3; 33pp; German.

Heine G;

Kruhoeffer M, Meyer M, Pardigol A,

Kist A,

Forssmann W,

WPI; 1997-290350/27.

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The present sequence is a carboxy-terminal fragment of the human correctivating peptide II (GCAP-II) precursor, prepared by consider cyclase activating peptide II (GCAP-II) precursor, prepared by endoptrotecloytic cleavage with endoptroteinase Arg-C. GCAP-II increases cGMP formation, and is involved in the control of transspithalial water and electrolyte transport. GCAP-II can be used to treat a variety of kidney, intestinal, respiratory, urogenital, circulatory and mervous system disorders, diseases of the endocrine and sensory systems (e.g. osteoporosis, and dental disease), disorders of the pancreas (e.g. osteoporosis, and dental disease), disorders of the pancreas (e.g. catabetes, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of diarrhoes, without inducing an immune treatment of category as ingene for the production of recombinant GCAP-II or thranged against GCAP-II or transgenic animal creation. Antibodies raised against GCAP-II are useful as immuneassay reagents GCAP-II, or a fragment, are administered at, c. e.g. 100-1200 microg/day by intravenous or intrammecular injection or 300 c.1200 microg/day subcutaneously. They may also be given orally, c. intransally synthesised, or isolated by chromatography from transformed eukaryotic or prokaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II, generation of cGMP was
                                                                                                               95DE-01028544.
95DE-01028544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-110032/11.
                                                                                                                                                                                                                                            (FORS/) FORSSMANN W.
03-AUG-1995;
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Pred. No. 3.9e-42;

Best Local Similarity

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Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with chymotrypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the mellitus type II, renal and intestinal disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenical apparatus, disorders of the cardiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GCAP II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP-I (99-15) cDNA are useful for diagnosis and treatment of the above disorders e.g. gene
   GCAP-II influences cGMP production
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                                           e.9
                                                                                                                                                                                                                               1 AASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLP
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                                                                                                                                                                       Gaps
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increased in a dose dependent manner. GCAP-II influences cGMP prod via a known receptor for heat stable enterotoxin. Other stomach, intestinal, pancreatic and liver cells also responded to GCAP-II, via changes in intracellular Ca2+ ion concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human.
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                                                                                                                                                                                                                                                                                                  61 AVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTGCL 108
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                                                                                                                                 Length 108;
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100.0%; Pred. No. 2.8e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                            AAW18484 standard; peptide; 84 AA
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                                                                                                                                               Best Local Similarity
Matches 108; Conserv
                                                                                             Sequence 108 AA;
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DB 2; Length 84;

76.9%; Score 445;

Sequence 84 AA;

Query Match

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The present sequence is a carboxy-terminal tragment of the numan graduence is a carboxy-terminal tragment of the numan curvating peptide II (GAP-II) precursor, prepared by endoproteolytic cleavage with chymotrypain. GCAP-II increases CGMP condoproteolytic cleavage with chymotrypain. GCAP-II increases CGMP condoproteolytic cleavage with chymotrypain. GCAP-II increases CGMP cleatrolyte transport. GCAP-II can be used to treat a variety of kidney, intestinal, respiratory, urogenital, circulatory and nervous system (e.g. disorders, diseases of the endocrine and sensory systems (e.g. clasoretes, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of diarrhoea, without inducing an immune cresponse. The GCAP-II cDNA can be used to treat the same conditions, clone the GCAP-II cDNA can be used to treat the same conditions, clone the GCAP-II cDNA can be used to treat the same conditions, clone the GCAP-II concoling gene for use in gene therapy, as a conditions, clone the GCAP-II concoling sensor araised against GCAP-II are useful as immunoassay reagents of the production of recombinant GCAP-II or cranspenit animal creation. Antibodies raised against CAP-II are useful as immunoassay reagents GCAP-II, new alway also be given orally.

CI 100-1200 microg/day by intravenous or intramuscular injection or 300 contranspenit control or prockaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II influences CGMP was concessed in a dose dependent manner. GCAP-II influences CGMP production via a known receptor for heat stable enterotoxin. Other stomach,
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                                                                                                                                                                                     1 IQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLFAVCHHPALPQDLQPVCASQEASSI
                                                                                                                                          29 IQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSI
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controls transport of water and electrolytes across epithelial cells.
                                                                         Gaps
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                                                                         Indels
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                                                                         Mismatches
                                                                                                                                                                                                                                                                                             89 FKTLRTIANDDCELCVNVACTGCL 112
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100.08; FA
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                                                                     84; Conservative
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                                                                         Matches
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XX AAW2

XX AAW2

XX AAW2

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32 QGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with chymotrypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenital apparatus, disorders of the cardiovascular and nervous systems, disorders of the integmments and sense organs and diseases associated with GCAP II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone.
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intestinal, pancreatic and liver cells also responded to GCAP-II, e.g. via changes in intracellular Ca2+ ion concentration
                                                                                                                                                                                    1 İQYĞGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSI
                                                                                                                                                              29 IQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSI
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human.
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                                                                                     Length 84;
                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GCAP-II (89-112) chymotrypsin digested fragment 2.
                                                                                     76.9%; Score 445; DB 2; I 100.0%; Pred. No. 3.9e-42; iive 0; Mismatches 0;
                                                                                                                                                                                                                                     89 FKTLRTIANDDCELCVNVACTGCL 112
                                                                                                                                                                                                                                                         61 FKTLRTIANDDCELCVNVACTGCL 84
                                                                                                                                                                                                                                                                                                                                                              AAW18485 standard; peptide; 81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 3; 33pp; German.
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                                                                                                                            84; Conservative
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                                                                                   Query Match
Best Local Similarity
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                                                         Sequence 84 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1998
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74.1%; Score 429; DB 2; Length 81; 100.0%; Pred. No. 2.4e-40; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 81; Conservative

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The present sequence is a carboxy-terminal fragment of the human curvature cyclase activating peptide II (GCAP-II) precursor, prepared by enapylate cyclase activating peptide II (GCAP-II) precursor, prepared by endoproteolytic cleavage with chymotrypsin. GCAP-II increases GGMP cormation, and is involved in the control of transepithelial water and formation, and is involved in the control of transepithelial water and clectrolyte transport. GCAP-II can be used to treat a variety of kidney, intestinal, respiratory, urogenital, circulatory and nervous system of sorters, and dental disease), disorders of the pancreas (e.g. cateoporosis, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of disorders of the pancreas (e.g. diabetes, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of diarrhoca, without inducing an immune conditions, clone the GCAP-II-encoding gene for use in gene therapy, as a fumunoassay reagents. GCAP-II, or a fragment, are administered at. ctranspent animal creation. Antibodies raised against GCAP-II are useful as immunoassay reagents. GCAP-II, or a fragment, are administered at. ce.g. 100-1200 microg/day by intravenous or intramsenal injection or 300 cc.g. intransally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-II was chemically synthesised, or isolated by chromatography from cransformed enkaryotic or prokaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II, generation of GGMP was corresponded in intracellular Ca2+ ion concentration
                                                                                                                                                                                                                                                                                                                                                                          Human; guanylate cyclase; activating peptide; GCAP-II; cGMP; transepithelial transport; treatment; kidney; intestinal; respiratory; urogenital; circulatory; nervous system; disorder; disease; endocrine; sensory; system; osteoporosis; dental; parcras; diabetes; hypophysis; gastrointestinal tract; diarrhoas; gene therapy; probe; recombinant production; transgenic animal; antibody; immunoassay reagent.
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Guanylate cyclase activating peptide II - increases cGMP formation, an controls transport of water and electrolytes across epithelial cells.
                                                                                                                                                                                                                                                                                                                                         GCAP-II C-terminal fragment prepared by chymotrypsin.
                                                                                                                                                                                                               AAW23233 standard; peptide; 81 AA
                                                                                        61 LRTIANDDCELCVNVACTGCL 81
                                                                92 LRTIANDDCELCVNVACTGCL
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Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with chymotrypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenital apparatus, disorders of the cardiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GCAP II (89-II2) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
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etc.
                                                                                                                         1 QGFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKT
                                                                                                 32 QGPRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKT
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heine
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                                    Length 81;
                           74.1%; Score 429; ..., 100.0%; Pred. No. 2.4e-40; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Human GCAP-II (89-112) chymotrypsin digested fragment 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New guanyl cyclase C activating peptide activity, useful for treating diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kruhoeffer M,
                                                                                                                                                                 92 LRTIANDDCELCVNVACTGCL 112
                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                     AAW18486 standard; peptide; 78 AA
                                                                                                                                                                                                  61 LRTIANDDCELCVNVACTGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 3; 33pp; German.
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                                                Similarity 100.
81; Conservative
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Sequence 81 AA;
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Best Local S
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Matches
                                                                                                                                                                                                                                                      RESULT 12
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The present sequence is a carboxy-terminal fragment of the human candinate cyclase activating peptide II (GCAP-II) precursor, prepared by endoproteolytic cleavage with chymotrypain. GCAP-II) precursor, prepared by comparing the control of transpital water and electrolyte transport. GCAP-II can be used to treat a variety of kidney, intestinal, reablization, and is involved in the control of transcpitalial water and electrolyte transport. GCAP-II can be used to treat a variety of kidney, cliseases of the endocrine and sensory systems (e.g. disperse, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of distribution inducing an immune the GCAP-II conciding gene for use in gene therapy, as a concition probe and for the production of recombinant GCAP-II or transgenic animal creation. Antibodies raised against GCAP-II are useful cas immunoassay reagents. GCAP-II, or a fragment, are administered at, e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300 contransmally or by inhalation, in typical unit doses of 0.3-30 mg. CCMP-II was chemically synthesised, or isolated by chromatography from transformed eukaryotic or prokaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II influences CGMP was increased in a dose dependent manner. GCAP-II influences CGMP production via a known receptor for heat stable enterotoxin. Other stomach, in the contract of GCAP-II, e.g.
transepithelial transport; treatment; Kidney; intestinal; respiratory; urogenital; circulatory; nervous system; disorder; disease; endocrine; sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis; gastrointestinal tract; diarrhoes; gent therapy; probe; recombinant production; transgenic animal; antibody; immunoassay reagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guanylate cyclase activating peptide II - increases cGMP formation, and controls transport of water and electrolytes across epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                   guanylate cyclase; activating peptide; GCAP-II; cGMP;
                                                                                                                                                                                                                                                                                                                         GCAP-II C-terminal fragment prepared by chymotrypsin.
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                                                                                                                                                                                                     AAW23234 standard; peptide; 78 AA
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                                                                                         61 IANDDCELCVNVACTGCL
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71.2%; Score 412; DB 2; Length 78; 100.0%; Pred. No. 1.9e-38;

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0; Indels

Sequence 78

Best Local Similarity 100. Matches 78; Conservative

Query Match

96 ANDDCELCVNVACTGCL 112

61 ANDDCELCVNVACTGCL

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                                                                                                                                                                                        1 RVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRT
                                                                                                                                                35 RVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRT
                                                                                  Gaps
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100.0%; Pred. No. 6.7e-38;
ive 0; Mismatches 0;
                   Score 412; DB 2; 1
Pred. No. 1.9e-38;
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71.2%; Sco. 100.0%; Pred. No. ... 0; Mismatches
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                                                                                  78; Conservative
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                   Query Match
Best Local Similarity
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peptides AAW18478-W18483 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with trypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, remal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenital apparatus, disorders of the respiratory. This peptide can he used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP il (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP il (99-15) cDNA are useful for diagnosis and treatment of the above disorders e.g. gene
                                                                                                                                                                                                                                                                                                                                                                                                                               New guanyl cyclase C activating peptide fragments - have insulinotropic activity, useful for treating diabetes, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 VQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                     Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic; diabetes; endocrine disorder; diagnosis; treatment; human.
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                                                                                                                                                                                                                                                                                                                                                                        Pardigol A,
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Pred. No. 6.7e-38;
0; Mismatches 0; Indels
                                                                                                       Human GCAP-II (89-112) trypsin digested fragment 2.
                                                                                                                                                                                                                                                                                                                                                                        Meyer M,
                                                                                                                                                                                                                                                                                                                                                                        Kruhoeffer M,
            AAW18479 standard; peptide; 77 AA.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 3; 33pp; German.
                                                                                                                                                                                                                                                                                                             95DE-01043628
                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy for diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-290350/27.
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nes 77; Conserv
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                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                             24-NOV-1995;
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                                                                                                                                                                                                                                                                              24-NOV-1995;
                                                                          22-APR-1998
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Matches 77;
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Search completed: March 26, 2005, 16:44:28 Job time : 122.628 secs

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VOLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTI

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77 QPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
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Matches 35; Conserv
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Sequence 5, Appli
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                                                                                                               March 26, 2005, 16:38:19 ; Search time 33.5182 Seconds (without alignments) 249.437 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 8148, Apple Sequence 14, Appl Sequence 10770, A Sequence 10770, A Sequence 21041, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22, Appli Sequence 21, Appli Sequence 21, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 115;
                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07903029
; Patent No. 5969097
; GENERAL INFORMATION:
APPLICANT: Wiegand, Roger C.
APPLICANT: Currie, Mark C.
APPLICANT: Fok. Kam F.
TITLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-489-039A-8148

US-09-059-625-74

US-09-905-625-74

US-09-902-510-10770

US-09-902-510-11681

US-09-252-991A-21041

US-09-270-767-42614

US-09-270-767-42614

US-08-778-428-4

US-08-778-428-2

US-08-778-428-2

US-08-778-428-2

US-08-778-428-2

US-08-778-428-2

US-08-778-428-2

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US-08-521-220-22

US-08-521-220-22

US-08-58-488-11
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TELBFAX: (314)694-9009
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 115 amino acids TYPE: AMINO ACID
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; MOLECULE TYPE: peptide
US-07-903-029-6
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28.1%; Score 162.5; DB 2; Length 115;
Best Local Similarity 36.1%; Pred. No. 1.1e-12;
Matches 35; Conservative 15; Mismatches 32; Indels 15
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US-07-903-029-6
; Sequence 6, Application US/07903029
; Patent No. 5969097
; GENERAL INFORMATION:
    APPLICANT: Wiegand, Roger C.
    APPLICANT: Currie, Mark C.
    APPLICANT: Currie, Mark C.
    APPLICANT: Currie, Mark C.
    APPLICANT: Currie, Mark C.
    APPLICANT: Por SEQUENCES:
    APPLICANT: SEQUENCES:
    APPLIC
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Currie, Mark C.
APPLICANT: Fok, Kam F.
TITLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/903,029
FILING DATE: 19920623
FILING DATE: 19920623
FLING DATE: 19920623
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 94,547
REFERENCE/DOCKET NUMBER: 07-21(872)A
TELEPHONE: (314,694-9009)
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
9 KPLCKEPNAQEILORLEEIAEDPGTCEICAYAACTGC 115
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          Sequence 5, Application US/07903029
Patent No. 5969097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 115 amino acida
TYPE: AMINO ACID
TOPOLOGY: linear
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                                             셤
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11 LLGALAVLV-----EGVTVQDGDLSFPLESVKQLKHLREVQ---EPTLMSHKKFALRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 -QSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.0%; Score 133; DB 2; Length 115; Best Local Similarity 32.2%; Pred. No. 6e-09; Matches 37; Conservative 16; Mismatches 40; Indels
CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,029
FILING DATE: 19920623
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET UNBER: 34,547
TELECOMMULCATION INFORMATION:
TELEPHONE: (314)694-5402
TURESTRATION: COMPANIEM TOWNER: TELEPHONE: (314)694-5402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Currie, Mark G.
APPLICANT: Currie, Mark G.
APPLICANT: Kita, Toshihiro
APPLICANT: Smith, Christine E.
APPLICANT: Fok, Kam F.
TITLE OF INVENTION: Human Uroguanylin
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STRETT: P. O. Box 5110
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STAMP PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,940
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NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 07-21(808)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08145940
Patent No. 5489670
GENERAL INFORMATION:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                    Query Match 16.6%; Score 96; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 1.8e-05; Matches 16; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: MOTGBETECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MATK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 33,229
TELECOMMUTCATION INFORMATION:
TELEPHONE: 215-568-3109
TELEPANS: 215-568-3109
TELEPANS: 215-568-3109
TELEPANS: 15-568-3109
TELEPANS: 15-568-3109
TELEPANS: 15-568-3109
TELEPANS: 15-568-3109
TELEPANS: 15-568-3109
SECOURMED FOR ERED IN O. 56:
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10S-08-281-447A-56
1 Sequence 56, Application US/08583447A
1 Patent No. 5879656
                                                                                                                                                                                                                                                                                                                  97 NDDCELCVNVACTGCL 112
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TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 16 amino acids amino acids
                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-145-940-1
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MOLECULE TYPE: peptide
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RESULT 6 US-08-145-940-2

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US-08-583-447A-55

US-08-583-447A-55

Sequence 55, Application US/08583447A

Patent No. 5879566

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%; Score 90; DB 1; Length 15; 100.0%; Pred. No. 9.5e-05;
                                                   APPLICANT: Currie, Mark G.
APPLICANT: Currie, Mark G.
APPLICANT: Smith, Christine E.
APPLICANT: Parent Farent Dept.
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STRATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 2, Application US/08145940
; Patent No. 5489670
; GENERAL,INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 07-2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
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SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DDCELCVNVACTGCL 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.C
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-145-940-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Sequence 7573, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 573

SEQ ID NO 573
                                                                                                                                                                                                                                                                                                                                                                                                                          41 MKKLSDLEAQWAPSPRLQAQSLLPAVCHHPAL--PQDLQPVCASQEASSIFKTLRTIAND 98
                                                                                                                                                                                                                                                                                                  Query Match 13.0%; Score 75; DB 4; Length 467; Best Local Similarity 33.3%; Pred. No. 0.9; Matches 25; Conservative 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%; Score 74.5; DB 4; 24.1%; Pred. No. 1.6;
                                                                                                                                                                                                                           ; OTHER INFORMATION: Rat Tpl2 polypeptide sequence US-09-522-775A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches
                   CURRENT APPLICATION NUMBER: US/09/522,775A CURRENT FILING DATE: 2000-03-08
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GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION:
FITLE OF INVENTION: KINASES
                                       CURRENT FILING DATE: 2000-03-0
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 467
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : || |:| ||| 416
416 ELELPENIADSSCTG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 DCELCVNVA---CTG 110
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Best Local Similarity 24.1:
Matches 26; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-7573
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION SAFERS: US/09/252, 991A
CURRENT PAPLICATION NUMBER: US 60/074, 788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19632
LENGTH: 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 GFRVQLESMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEASSIFKTL 92
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APPLICANT: Tsichlis, Philip N.
TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases FILE REFERENCE: OTT-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.5; DB 4; Length 1206;
Pred. No. 0.68;
6; Mismatches 34; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 0.0013;
...hea 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 17UT-1702
TELEPHONE: 215-568-3190
TELEPHONE: 215-568-3199
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 81; 85.7%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19632, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09522775A
Patent No. 6660906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.5%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 DDCELCVNVACTGC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-583-447A-55
                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 12; Conserv
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US-09-522-775A-4
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12 GVAVVLLLLLQSTQSVYIQYQGFRVQLESM------KKLSDLEAQWAPSPRLQAQ 60
                                                                                                                         33;
                                                                                                                                                                                  61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVAC 108
                                                                                                                                                                                                               :|::||:
193 --IPSLCHYAF-----PYC--DETSSVPKP-RDLCRDECEILENVLC 229
Length 623;
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12 GVAVVLLLLLLQSTQSVYIQYQGFRVQLESM------KKLSDLEAQWAPSPRLQAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 GIACARFI --- GNRTVYMESLHMQGEIENQITAAFTMIGTSSHLSDKCSQFA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVAC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.9%; Score 74.5; DB 2; Length 800; Best Local Similarity 24.1%; Pred. No. 2.2; Matches 26; Conservative 20; Mismatches 29; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Regeneron Pharmaceuticale, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-469-537A-105
; Sequence 105, Application US/08469537A
; Patent No. 5843749
; GENERAL INSAMTION:
; TILLE OF INVENTION: EHK AND ROR TYROSINE
; TITLE OF INVENTION: KINASES
; TUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-0CT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-0JU-1991
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: 32,143
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONS: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
OSTWARE: FASESBO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-UIN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
APPLICATION NUMBER: 26-UIL-1991
ATTORNEY/AGENT INFORMATION:
06-JUN-1995
06-JUN-1995
07: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 800 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-537A-78
         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                  APPLICATION NUMBER:
FILING DATE: 06-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVAC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.9%; Score 74.5; DB 2; Length 800; Best Local Similarity 24.1%; Pred. No. 2.2; Matches 26; Conservative 20; Mismatches 29; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-469-537A-78

Sequence 78, Application US/08469537A

Sequence 78, Application US/08469537A

Patent No. 5843749

GENERAL INFORMATION:
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown

STATE: NY
         3: Regeneron Pharmaceuticals, Inc.
777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GVAVVLLLLLQSTQSVYIQYQGFRVQLESM---
                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSEEG VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-UUL-1991
ATTORNEY, AGENT INFORMATION:
NAME: Kempler, Ph. D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION NUMBER: REG 14-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ANDIUM TYPE: DISKETTE
THERE: TBM COMPALIBLE
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 800 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                        STREET: ///
                                                                                                   U.S.A.
         ADDRESSEE:
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                                                                                                   COUNTRY:
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Gaps

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Search completed: March 26, 2005, 16:51:13
Job time : 34.5182 secs
                               CURRENT FILING DATE: 2000-03-C
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 467
                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : || |:| |||
416 ELELPENIADSSCTG 430
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: GATS L. SOUR SECOS-03PA
CURRENT APPLICATION NUMBER:
NUMBER OF SEC ID NOS: 8252
NUMBER OF SEC ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GVAVVLLLLLQSTQSVYIQYQFRVQLESM------KKLSDLEAQWAPSPRLQAQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases
FILE REFERENCE: OTT-1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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175 GIACARFI---GNRTVYMESLHMQGEIENQITAAFTMIGTSSHLSDKCSQPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVAC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 12.9%; Score 74.5; DB 2; Length 937; 1 Similarity 24.1%; Pred. No. 2.7; 26; Conservative 20; Mismatches 29; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 73.5; DB 4; 31.7%; Pred. No. 0.45; tive 12; Mismatches 35;
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-145-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: : | | :| | 128 VTRADIEQIRGVSNNSQILRTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ALPODLOPVCASQEASSIFKTL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-522-775A-2
Sequence 2, Application US/09522775A
Patent No. 6660906
GENERAL INFORMATION:
                                                                                                                                         INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 937 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.78
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: Human ROR1
                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1...937; OTHER INFORMATION: US-08-469-537A-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-328-352-4746
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41 MKKLSDLEAQWAPSPRLOAQSLLPAVCHHPAL--PQDLOPVCASQEASSIFKTLRTIAND 98
                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.4%; Score 72; DB 4; Length 467; Best Local Similarity 32.0%; Pred. No. 2.2; Matches 24; Conservative 16; Mismatches 25; Indels
                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Human Tpl2 polypeptide sequence
US-09-522-775A-2
CURRENT APPLICATION NUMBER: US/09/522,775A CURRENT FILING DATE: 2000-03-08
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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March 26, 2005, 16:48:40; Search time 111.591 Seconds (without alignments) 332.314 Million cell updates/sec
- protein search, using sw model
  OM protein
                                             Run on:
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1 MGCRAASGLLPGVAVVLLLL......RTIANDDCELCVNVACTGCL 112 US-10-775-481A-56 579 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1407402 segs, 331100923 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO7 \) \text{PUBCOMB.pep:*} \\
2: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PME VUB.pep:*} \\
3: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PME VUB.pep:*} \\
4: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
5: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
7: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
9: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
10: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
11: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
13: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
13: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
13: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
16: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.pep:*} \\
17: \( cgn2 \frac{6}\) \text{prodata} \( 1/\) \text{pubpaa} \( USO \frac{6}\) \text{PUBCOMB.p

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result		Querv				
No.	Score	Match	Match Length DB ID	DB	ID	Description
1	579	100.0	112	17	US-10-479-606-5	Sequence 5, Appli
7	252	43.5	109	17		Sequence 6, Appli
m	216	37.3	85	σ	_	Sequence 1527, Ap
4	216	37.3	85	10	US-09-925-299-1527	Sequence 1527, Ap
Ŋ	162.5		115	O	_	Sequence 61, Appl
9	162.5		115	14	US-10-235-994-22	Sequence 22, Appl
7	162.5		115	14	US-10-262-473-12	Sequence 12, Appl
œ	162.5		115	17	US-10-479-606-4	Sequence 4, Appli
0	136		108	14	US-10-262-473-16	Sequence 16, Appl
2	132		102	14	US-10-262-473-14	Sequence 14, Appl
11	96		16	14	US-10-107-814-1	Sequence 1, Appli
12	96		16		US-10-197-954-141	Sequence 141, App
13	96		16	15	US-10-621-684-56	Seguence 56. Appl

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US-10-479-606-2 US-10-760-085-141 US-10-10-814-20 US-09-925-299-1162 US-09-925-299-1162 US-10-61-684-55 US-10-61-684-55 US-10-10-814-21 US-10-28-075-245 US-09-374-579-2 US-09-374-579-2 US-09-374-598-12 US-10-374-414-4 US-10-387-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2 US-10-287-226-2	US-10-287-226-19 US-10-287-226-18 US-10-287-226-4 US-10-287-226-4 US-10-287-226-16 US-10-287-226-12 US-10-287-226-10 US-10-287-226-10
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## ALIGNMENTS

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Sequence 5, Application US/10479606

Publication No. US20050032684A1

GENERAL INFORMATION:

APPLICANT: Cetin, Yalcin

APPLICANT: Savas, Yuksel

TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

FILE REFERENCE: 03100192aa

CURRENT PRILING DATE: 2003-12-04

PRIOR APPLICATION NUMBER: DE10127119.0

PRIOR APPLICATION NUMBER: PT/DE02/02040

PRIOR PILING DATE: 2002-06-05

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.2

LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: homo sapiens
US-10-479-606-5
-10-479-606-5
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LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                              LOCATION: (132)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1527
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1527, Application US/09925299; Publication No. US20030040617A9; GENERAL INFORMATION: APPLICANT: Rosen et al.
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71 XLLAAVCHHPAL 82
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OTHER INFORMATION:
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LOCATION: (70)
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (34)
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                                                            Sequence 6, Application US/10479606

Publication No. US20050032684A1

GENERAL INFORMATION

APPLICANT: Cetin, Yalcin

APPLICANT: Cetin, Yalcin

TITLE OF INVENITON: Guantylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENITON: Cananylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENITON: Cananylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENITON: Cananylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENITON: Cananylate-cyclase C ligand, administered via the airways, for the

TITLE OF INVENITON WUMBER: US 1200.404

PRIOR FILING DATE: 2003-12-04

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 6

LEASTHALE PARENTH: 109

LEASTHALE PARENTH: 109
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids.
NAMB/KEY: SITE
LOCATION: (29)
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OTHER INFORMATION: Kaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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43.5%; Score 252; DB 17; Length 109;
Best Local Similarity 50.5%; Pred. No. 4.9e-21;
Matches 52; Conservative 17; Mismatches 32; Indels 3
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Fatent No. US20020055627A1
GENERAL INFORMATION:

APPLICANT: ROSen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILER REFERENCE: PA.02
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05883
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 HHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCVNVACTG 110
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ORGANISM: Homo sapiens
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; ORGANISM: oppossum
US-10-479-606-6
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NAME/KEY: SITE
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ORGANISM: Homo sapiens
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US-09-981-353-61
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 1090-03-03
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ IN DOS: 1556
SOFTWARE: PATENTIN VOR: 2.0
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OTHER INFORMATION: Xaa equals any
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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OTHER INFORMATION:
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LOCATION: (70)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                    LOCATION: (71)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEX: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1527
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Publication No. US20030101002A1
GENERAL INFORMATION:
APPLICANT: Bartha, Gabor
APPLICANT: Walker, Michael
TITLE OF INVENTION: WETHODS FOR ANALYZING GENE EXPRESSION PATTERNS
FILE REFERENCE: ICYTP012
CURRENT APPLICATION NUMBER: US/10/235,994
CURRENT FILING DATE: 2002-09-04
PRIOR PLILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/245,081
PRIOR FILING DATE: 2000-11-01
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                                                                                                                                                                                                                                              Length 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEX: misc feature
NOTHER INFORMATION: Incyte ID No. US20020160382A1 1800311CD1
US-09-981-353-61
                                                                                                                                                                                                                                                                                              Indels
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Fatent No. US20020160382A1
GENERAL INPORMATION:
APPLICANT: Lasek, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 QPVCASQEASSIFKTLRTIAND - - DCELCVNVACTGC 111
                                                                                                                                                                                                                                           Score 216; DB 10;
Pred. No. 5.1e-17;
3; Mismatches 24;
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.5%;
Matches 45; Conservative 3
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Sequence 4, Application US/10479606

Publication No. US20050032684A1

GENERAL INFORMATION:

APPLICANT: Catin, Valcin

APPLICANT: Savas, Yuksel

TITLE OF INVENTION: Lreatment of respiratory airway problems

TITLE OF INVENTION: Lreatment of respiratory airway problems

TITLE OF INVENTION: Lreatment of respiratory airway problems

TURENT APPLICATION NUMBER: US/10/479,606

CURRENT APPLICATION NUMBER: DS10127119.0

PRIOR APPLICATION NUMBER: DC1027119.0

PRIOR PILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 7

SOFFWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AQWAPSPRLQAQSLLPAVCHHPALPQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.1%; Score 162.5; DB 17; Length Best Local Similarity 36.1%; Pred. No. 1.2e-10; Matches 35; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 OPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 4
; LENGTH: 115
; TYPE: PRT
; ORGANISM: rat or homo sapiens (guanylin)
US-10-479-606-4
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APPLICANT: Burgess, Catherine,
APPLICANT: Burgess, Catherine,
APPLICANT: Burgess, Catherine,
APPLICANT: Gorman, Linda,
APPLICANT: Gorman, Linda,
APPLICANT: Gorman, Linda,
APPLICANT: Gorman, Linda,
APPLICANT: Reiger, Denise,
APPLICANT: Reiger, Daniel,
APPLICANT: Spyeek, Kimberly,
APPLICATION NUMBER: 00/320,030
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-39
                                                                                                                                                                                                                                                                                                            'n.
                                                                                                                                                                                                                                                                                                                                                   27 VYIQYQGFRVQLESMKKLSDLE-----AQWAPSPRLQAQSLLPAVCHHPALPQDL 76
                                                                                                                                                                                                                                                                                                                                                                                       22 VIVQDGNFSFSLESVKKLKDLQEPRVGKLRNFAPIP---GEPVVPILCSNPNFPEEL 78
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                                                                                                                                                                                                                                   Query Match 28.1%; Score 162.5; DB 14; Length 115; Best Local Similarity 36.1%; Pred. No. 1.2e-10; Matches 35; Conservative 15; Mismatches 32; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 OPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 OPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 115
LYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 VYIQYQGFRVQLESMKKLSDLE----
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Publication No. US20030199442A1
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Best Local Similarity 36.1%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            US-10-235-994-22
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US-10-479-606-4
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23.5%; Score 136; DB 14; Length 108;

Query Match

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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 141, Application US/10197954

Publication No. US20030119021A1

GENERAL INFORMATION:
APPLICANT: Siddid, Subaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24742-2305
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT FILING DATE: 2002-07-16
FRIOR FILING DATE: 2001-07-16
FRIOR FILING DATE: 2001-08-21
FRIOR FILING DATE: 2001-08-21
FRIOR FILING DATE: 2001-08-21
FRIOR FILING DATE: 2001-08-31
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US-10-621-684-56
Sequence 56, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
HAPLICANT: Waldman, Scott A.
TITLE OF INVENTION:
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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100.0%; Pred. No. v.
      CURRENT APPLICATION NUMBER: US/10/107,814
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Sc.
illarity 100.0%; P.
Conservative 0;
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapien
US-10-197-954-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                     ; LOCATION: (4)..(12)
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
US-10-107-814-1
                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-197-954-141
                                                                                                                                                          LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
                                                                                         27 VYIQYQGFRVQLE-SMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEA 85
                                                                                                                                 25 VTVQDGNFSFSLEPRVGKLRN---FAPIP---GEPVVPILCSNPNFPEELKPLCKEPNA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 VYIQYQGFRVQLE-SMKKLSDLEAQWAPSPRLQAQSLLPAVCHHPALPQDLQPVCASQEA 85
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APPLICANT: NIKIFOROVICH, GREGORY
APPLICANT: NIKIFOROVICH, GREGORY
APPLICANT: JACOB, GARY S.
TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS
FILE REFERENCE: 81361/284943/MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                     Indels
Best Local Similarity 36.0%; Pred. No. 1.2e-07; Matches 32; Conservative 15; Mismatches 32
                                                                                                                                                                                                               86 SSIFKTLRTIAND--DCELCVNVACTGCL 112
                                                                                                                                                                                                                                                 86 SSIPKTLRTIAND -- DCELCVNVACTGC 111
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PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR PILING DATE: 2001-10-29
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: CuraSeqList version 0.1
SEG ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/10262473
Publication No. US20030199442A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alsobrook, John,
APPLICANT: Burgess, Catherine,
APPLICANT: Gorman, Linda,
APPLICANT: Guo, Xiaojia,
APPLICANT: Lepley, Denise,
APPLICANT: Rastelli, Luca,
APPLICANT: Rastelli, Luca,
APPLICANT: Restelli, Luca,
APPLICANT: Spytek, Kimberly,
APPLICANT: Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 21402-462B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-262-473-14
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RESULT 15
US-10-760-085-141
i Sequence 141, Application US/10760085
i Publication No. US2005042771A1
i GENERAL INFORMATION:
i APPLICANT: Hubert K"ster
i APPLICANT: Suhaib Mahmod Siddiqi
APPLICANT: Subramaniam Marappan
i APPLICANT: Subramaniam Marappan
i APPLICANT: Subramaniam Marappan
i APPLICANT: Subramaniam Marappan
i APPLICANT: Ping Yip
i TITLE OF INVENTION: Capcure Compounds, Collections Thereof
i TITLE OF INVENTION: Capcure Compounds
i TITLE OF INVENTION: Capcure Compounds
i TITLE OF INVENTION: Capcure Compounds
i TITLE OF INVENTION: Capcositions
i TITLE OF INVENTION: Capcositions
i TITLE OF INVENTION: Capcositions
i CURRENT APPLICATION NUMBER: 105/41,398
i CURRENT PILING DATE: 2004-01-16
i PRIOR APPLICATION NUMBER: 60/441,398
i PRIOR APPLICATION NUMBER: 60/441,398
i MANDED ADE 2003-01-16
i NUMBER AD AD ALL ADD ALL AD  ALL AD  ALL AD ALL A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: March 26, 2005, 17:16:38 Job time : 111.591 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 NDDCELCVNVACTGCL 112
                      1 NDDCELCVNVACTGCL 16
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Cetin, Yalcin
APPLICANT: Savas, Yuksel
TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via
TITLE OF INVENTION: Lreatment of respiratory airway problems
TITLE OF INVENTION: Lreatment of respiratory airway problems
TITLE OF INVENTION: Leatment of respiratory airway problems
FILE REFERENCE: 03100192aa
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: DE10127119.0
PRIOR APPLICATION NUMBER: PCT/DE02/02040
PRIOR APPLICATION NUMBER: PCT/DE02/02040
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 16
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16.6%; Score 96; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Worderfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-203
CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INDEMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMULCATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 56: US-10-621-684-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10479606
Publication No. US20050032684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acidd
TYPE: amino acid
                                 STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 NDDCELCVNVACTGCL 112
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Philadelphia
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-479-606-2
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97 NDDCELCVNVACTGCL 112

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Gaps

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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protein search, using sw model OM protein March 26, 2005, 16:37:49; Search time 23.708 Seconds (without alignments) 454.541 Million cell updates/sec Run on:

US-10-775-481A-56 579 1 MGCRAASGLLFGVAVVLLLL......RTIANDDCELCVNVACTGCL 112 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 88 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
	Score	Query	Length	DB	ID	Description
-	579	100.0	112	7	JC4651	uroguanylin precu
7	162.5	28.1	115	Н	A46279	quanylin precurso
e	161	27.8	116	~	JC7620	
4	153.5	26.5	116	٦	B46279	
2	133	23.0	115	٦	JN0318	
9	81	14.0	72	٦	QHECIB	heat-stable enter
7	76.5	13.2	200	7	B86312	type 2A protein s
æ	75	13.0	467	~	A47388	serine/threonine
6	74.5	12.9	937	7	A45082	neurotrophic rece
10	74	12.8	72	Н	QHEC4	heat-stable enter
11	74	12.8	467	7	149609	proto-oncogene pr
12	74	٦	824	~	150618	c-fps proto oncog
13	72,		467	~	A48713	serine/threonine-
14	71,	12.3	737	N	863453	probable RNA heli
15	68.5	11.8	369	~	AG0386	5-amino-6- (5-phos
16	68.5	11.8	669	~	T18984	hypothetical prot
17	68	11.7	873	-	TVFVFS	protein-tyrosine
18	66.5	11.5	538	~	AC1850	NADH dehydrogenas
19	66.5	11.5	1127	N	T21635	hypothetical prot
20	99	11.5	1165	~	T21636	
21	99	11.4	580	~	T43485	
22	65.5	11.3	144	~	C70937	
23	v	11.3	322	~	D86760	phosphate starvat
24	65.5	11.3	533	-	TVFVFP	protein-tyrosine
25	65	11.2	710	~	T52573	cyclic nucleotide
56	64.5	11.1	211	N	D82109	outer membrane li
27	64.5	11.1	367	ď	F82098	riboflavin-specif
28	64.5	11.1	378	~	B89588	protein R09F10.7
53	64.5	11.1	488	~	S13423	stromelysin 3 (EC

hypothetical prote NADH2 dehydrogenas	ribonuclease inhib polyadenylate-bind	hypothetical prote RNA helicase TNZ2	probable RND-famil	paired-box contain	hypothetical prote	hypothetical prote	origin recognition	adenylate cyclase	unknown protein Tl	ribosomal protein	flagellar biosynth	flagellar biosynth
T00391 T12307	A31857 S41644	T28683 I48385	AD0771	JC5827	T50005	T29895	T40070	S24981	H96747	A27166	E90952	A85801
0 0	0 0	7 7	~	N	N	~	N	~	~	~	~	0
1736 344	456 465	537	1040	349	445	589	707	848	1088	96	692	692
11.11	111	111	11.1	11.0	11.0	11.0	11.0	11.0	11.0	10.9	10.9	10.9
64.5 64	64 64	64	64	63.5	63.5	63.5	63.5	63.5	63.5	63	63	63
	O1 00	44 N	9	7	<b>~</b>	σ.	0	_	۵.	43	47	10

# ALIGNMENTS

uroguanylin precursor - human N/Alternate names: guanylyl cyclase activating peptide II

C; Species: Homo sapiens (man)

Cidate: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004
CjAccession: JC4651; S63702; S68052
R;Miyazato, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, Biochem. Biophys Res. Commun. 219, 644-648, 1996
A;Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanyl A;Reference number: JC4651; MuID:96193705; PMID:8605041

A; Molecule type: mRNA A; Residues: 1-112 <MIY>

A; Cross-references: UNIPROT:Q16661; GB:U34279; NID:g1236798; PIDN:AAC50416.1; PID:g12367 R; Hill, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G. Biochim. Biochim. Biophys. Acta 1253, 146-149, 1995
A; Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precur A; Reference number: S63702; WUID:96106424; PMID:8519795

A;Accession: S63702
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Esperimental source: Lissue colon
A;Experimental source: tissue colon
B;Hess, R; Kuhn, M; Schulz-Knappe, P; Raida, M; Fuchs, M; Klodt, J; Adermann, K;
FEBS Lett. 374, 34-38, 1995
A;Title: GCAP-II: isolation and characterization of the circulating form of human urogus
A;Reference number: S68052; MUID:96049550; PMID:7589507

A;Accession: S68052

A;Molecule type: protein A;Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES> C;Comment: This protein, a member of the guanylin peptide family, is an endogenous activ

C; Keywords: intestine F;1-26/Domain: signal sequence #status predicted <SIG> F;27-112/Product: uroguanylin #status predicted <MAT>

C; Superfamily: guanylin

1 4 4 4 4 4 6 8 0 8 6 6 6 8 6 7 8 6 4 8 6 6 6 6 4 4 7 9 H

Gaps ö Length 112; Indela 100.0%; Score 579; DB 2; ilarity 100.0%; Pred. No. 4.1e-54; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 112; Conserv

1 MGCRAASGLLPGVAVVLLELLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 1 MGCRAASGLLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPSPRLQAQ 셤 à

9 9

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RESULT 2

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sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           guanylin precursor - mouse
C;Species: Mus musculus (house mouse)
                                                                                                                                                  Query Match
Best Local Similarity 39.4%;
Matches 43; Conservative
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Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A55643
7;1-28/Domain:
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                     Gradylin Precursor (waited) - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Stees-1993 # Bequence revision 26-May-1995 #text_change 09-Jul-2004
C; Accession: A64279; S29228; S298079, S29228; S298079, S29228
R; de Sauvage, F.G.; Kebbay, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
Proc. Natl. Acad. Sci. US.A. 89, 90839-9093, 1992
A; Title: Precureor structure, expression, and tissue distribution of human guanylin.
A; Reference number: A46279; MUD:93028409; PMID:1409606
A; Molecule type: mRNA
A; Residues: 1-115. 2DE1
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Mole: sequence extracted from NCBI backbone (NCBIN:115377, NCBIP:115378)
A; Reference number: S2920; MUD:9301964; PMID:1327879
A; Molecule type: mRNA
A; Raida, M.; Adermann, K.; Schulz-Knappe, P.; Gerzer, R.; Heim, J.M.; Forssmann
A; Residues: 1-115 cwtls
A; Molecule type: protein
A; Residues: 22-68 cwtls
A; Molecule type: protein
A; Residues: deceptor:
C; Comment: Garaylin is an endogenous ligand for an intestine-epecific receptor guanylyl
A; Anne, structure.
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A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Rossidues: 1-116 <COM>
A,Cross-references: GB:AJ301673
C,Comment: This protein, a member of a family of heat-stable peptides, is a potent extra
axis. This peptide signalling system plays a role in osmoregulation in euryhaline telec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 guanylin precursor, long form - Buropean eel
Cispecies: Anguilla anguilla (Buropean eel)
Cispecies: Anguilla anguilla (Buropean eel)
Cispacesion: JC7820
Cispacesion: JC7820
Ricomrie, M.M.; Cutler, C.P.; Cramb, G.
Biochem. Biophys. Res Commun. 281. 1078-1085, 2001
A; Title: Cloning and expression of guanylin from the Buropean eel (Anguilla anguilla).
A; Reference number: JC7620; MUID:21139737; PMID:11243845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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nes 32;
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C;Keywords: hormone; intestine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: guanylin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: guanylin
Keywords: heat-stable protein; osmoregulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GDB:136460; OMIM:139392
A,Map position: 1p35_1p34
              lanylin precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
35; Conserv
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Best Local &
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A; Molecule type: DNA
A; Residues: 1-116 <SC1.>
A; Residues: 1-116 <SC1.>
A; Cross-references: UNIPROT: P33680; GB: U60528; GB: U09741; NID: g1480667; PIDN: AAB05758.1;
R; de Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
A; Title: Precursor structure, expression, and tissue distribution of human guanylin.
A; Reference number: A46279; MUID: 93028409; PMID: 1409606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  guanylin precursor - rat
Gispedies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
CiAccession: JN0318; A43345; Ā38184; A38189
R;Wiegand, R.C.; Kato, J.; Currie, M.G.
Biochem. Biophys. Res. Commun. 185, 812-817, 1992
A;Title: Rat guanylin cDNA: characterization of the precursor of an endogenous activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-116 aDEL>
A;Cross-references: GB:M95175; NID:g309282; PIDN:AAA37758.1; PID:g309283
A;Cross-references: GB:M95175; NID:g309282; PIDN:AAA37758.1; PID:g309283
A;Note: sequence extracted from NCBI backbone (NCBIP:115379)
C;Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
C;Genetics:
                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 AVVLLLL----LQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAPS----PRLQAQSLLPA
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LLPGVAVVLLLLLQSTQSVYIQYQGFRVQLESMKKLSDLEAQWAP-----SPRLQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
F;29-116/Product: guanylin precursor, long form #status predicted <MAT>F;33-39/Region: homologous #status predicted
F;69-114/Region: highly conserved #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLLPAVC-HHPALPQDLQPVCASQEASSIFKTLRTIAND--DCELCVNVACTGC 111
                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                   68 VCSNPHLPAEFLPVCEREGASALFNRLVDIITPPDPCEICANAACTGCL 116
                                                                                                                                                                                                                                                                                                                                      66 VCHHPALPQDLQPVCASQEASSIFKTLRTIAN--DDCELCVNVACTGCL 112
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                                                                                                                    Length 116,
                                                                                                                                                                         Indels
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C;Kaywords: hormone; intestine
F;1.21/Domain: signal sequence #status predicted <SIG>
F;22-116/Product: guanylin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                 27.8%; Score 161; DB 2; 39.4%; Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.5%; Score 153.5; DB 1
36.8%; Pred. No. 4.8e-09;
live 13; Mismatches 40
                                                                                                                                      39.4%; Pred. ...
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us-10-775-481a-56.rpr

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A,Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
R;Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
Eur. J. Biochem. 129, 257-263, 1982
A;Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigeni
A;Reference number: A33067; MUID:83105138; PMID:6759126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cjaccesion: B8312
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: Aselili, MUD:21016719; PMID:11130712
A;Accession: B86312
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                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
A;Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type 2A protein serine/threonine phosphatase 55K regulatory chain F11A6.6 - Arabidopsis C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: enterotoxin; heat-stable protein
F;1-53/Domain: signal sequence and propeptide #status predicted <SIG
F;54-72/Product: heat-stable enterotoxin ST-1D #status experimental
F;59-64,60-68,63-71/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 PODAKPVESSKEKITLESKKCNIAKKSNKSGPESMNSSNYCCELCCNPACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 81; DB 1; Pred. No. 0.14; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%; Score 76.5; DE 26.6%; Pred. No. 3.2; iive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 PODLOPVCASQEASSIFKTLRTIA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: heat-stable enterotoxin ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%;
        A;Residues: 1-18,'A',20-72 <DWA>
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Best Local Similarity 37.74
Matches 20; Conservative
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A;Residues: 1-500 <STO>
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                                               A, Molecule type: mRNA
A, Recession: J.115 < WIED.
A, Rocession: J.115 < WIED.
A, Recession: J.115 < WIED.
A, Cross-references: UNIPROT.P28902; GB.N93005; NID:g204540; PIDN:AAA41300.1; PID:g204541
B; Schulz, S.; Chrisman, T.D.; Garbers, D.L.
J. Biol. Chem. 267, 16019-16021, 1992
A; Title: Cloning and expression of guanylin. Its existence in various mammalian tissues.
A; Receince number: A43345; MUID:g235545; PMID:1379587
A; Receince number: A43345; MUID:g204542; PIDN:AAA41302.1; PID:g204543
A; Receince: Had: Asid: May Mid: A; Molecule type: mRNA
A; Receince: L-115 < AGGHA
A; Receince: Carrected from NEB backbone (NCBIN:110474, NCBIP:110476)
B; Currie, M.G.; Pok, K.F.; Kato, J.; Moore, R.J.; Hamra, P.K.; Duffin, K.L.; Smith, C.B.
A; Reference number: A38184; MUID:g2141235; PMID:1346555
A; Arcession: A38184; MUID:g2141235; PMID:1346555
A; Roce equence: extracted from NCBI backbone (NCBIP:79480)
A; Note: equence extracted from NCBI backbone (NCBIP:79480)
A; Note: purification included boiling in acetic acid; peptide has activity but may repre where the EMBL Data Library, August 1992
A; Note: equence extracted from NCBI backbone (NCBIP:79480)
A; Note: equence extracted from A; Reference number: S25489
A; Note: equence extracted from a noted of an intestine-specific receptor quanylyl of the same receptor.
C; Comment: Guanylin is an endogenous ligand for an intestine-specific receptor quanylyl of C; Repertently; quanylin (C; Reported Hatatus predicted AMT>
F; 1-21/Domain: signal sequence #status predicted AMT>
F; 22-115/Product: quanylin #status predicted AMT>
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C; Species : Becherichia coli

C; Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004

C; Accession: JS0292, A33068; A33067; A30557

R; Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.

Infect: Immun. 39, 1167-1174, 1983

A; Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterot

A; Reference number: JS0292; MUID:83184648; PMID:6341230

A; Residues: 1-72 cMOS>

A; Residues: 1-72 cMO
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Reference number: JN0318; MUID:92328783; PMID:1378267
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Best Local Similarity 32.2'
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C;Species: Escherichia coli
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Datesion: JTG73; A35578
R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; F.
Plasmid 20, 42-53, 1988
A;Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheric
A;Reference number: JT0373; MUID:89202548; PMID:3071819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stable A;Reference number: A35978; MUID:90273381; PMID:2190361
A;Accession: A35978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P07965; GB:J03311; NID:g147875; PIDN:AAA24652.1; PID:g147876
R;Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure and tissue-specific expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q07174; GB:D13759; NID:g286072; PIDN:BAA02905.1; PID:g286073 A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 MKKLSDLEAQWAPSPRLOAQSLLPAVCHHPAL--PQDLQPVCASQEASSIFKTLRTIAND 98
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
Cispeciesion: 149609
Riohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
Jpn. J. Cancer Res. 84, 518-525, 1993
Airitle: The murine cot proto-oncogene : genome structure and tissue-specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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---PYC--DETSSVPKP-RDLCRDECEILENVLC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: estA4
C;Superfamily: heat-stable enterotoxin ST
C;Superfamily: heat-stable enterotoxin ST
C;Reywords: enterotoxin; heat-stable protein
C;Reywords: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <PRO>F;20-53/Domain: propeptide #status predicted <PRO>F;54-72/Product: heat-stable enterotoxin #status predicted <PRO>F;59-64,60-68,63-71/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.8%; Score 74; DB 2; Length 467; l Similarity 32.0%; Pred. No. 5.5; 24; Conservative 17; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 72;
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                                                                                                                                                                                    heat-stable enterotoxin STA4 precursor - Escherichia coli
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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12.8%; Score 74; DB 1;
Best Local Similarity 36.5%; Pred. No. 0.75;
Matches 19; Conservative 5; Mismatches
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--IPSLCHYAF---
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A, Residues: 1-72 <STI>
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A;Residues: 1-72 <ZHO>
C;Genetics:
224
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Best Local {
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R;Patriotis, C.; Makris, A.; Bear, S.E.; Tsichlis, P.N.
Proc. Natl. Acad. Sci. US.A. 90, 2251-2255, 1993
A;Title: Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved in the progression. A7388 MUID:93211939; PMID:7681591
A;Accession: A47388
A;Accession: A47388
A;Accession: A7388
A;Accession: A7388
A;Accession: A77388
A;Accession:
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A,Cross-references: GDB:136453
A,Cross-references: GDB:136453
A,Cross-references: GDB:136453
C,Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology; procyclemily: neurotrophic receptor ror; immunoglobulin homology; procyclemily: neurotrophic receptor spreadicted control from type files.
F;24-937/Product: neurotrophic receptor ror! #status predicted control from type files.
F;24-133/Domain: immunoglobulin homology cIMM>
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neurotrophic receptor rorl precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45082
J: Biol. Chem. 267, 26181-26190, 1992
A;Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A;Reference number: A45082; MUID:93100347; PMID:1334494
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F;404-425/Domain: transmembrane #status predicted <TM1>
F;471-753/Domain: protein kinase homology <KIN>
F;47,66,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                         Species: Rattus norvegicus (Norway rat)
Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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A;Residues: 1-937 <MAS>
A;Cross-references: UNIPROT:Q01973; GB:M97675; NID:g337464;
A;Note: sequence extracted from NCBI backbone (NCBIP:120916)
C;Genetics:
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24.1%; Pr.
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416 ELELPENIADSSCTG 430
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                                                                                  serine/threonine protein
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Best Local Similarity
Matches 25; Conserv
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A;Cross-references: EMBL:Z14138; NID:g31244; PIDN:CAA78512.1; PID:g31245
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416 ELELPENIADSSCTG 430
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                                                                                                           C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. State: 136.018
A; Mucleotide sequence and topography of chicken c-fps. Genesis of a retroviral on A; Reference number: 150618; MUID: 85160839; PMID: 3879969
A; Tatle: Nucleotide sequence and topography of chicken c-fps. Genesis of a retroviral on A; Reference number: 150618; MUID: 85160839; PMID: 3879969
A; Reference number: 150618
A
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Nylternate names: cot proto-oncogene, 58K form
C;Species: Home sapiens (man)
C;Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 07-Apr-1994 #sequence revision 17; Sumida, S.; Akiyama, T.; Toyoshima, K.
J Biol. Chem. 268, 22723-22732, 1993
A;Title: The human cot proto-oncogene encodes two protein serine/threonine kinases with A;Reference number: A48713; MUID:94043034; PMID:8226782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 30-467 <AO2>
A; Experimental source: TCO-4 cells
A; Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBIP:138972)
A; Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBIP:138972)
B; Chan, A.M.; Chedid, M.; Aaronson, S.A.; Miki, T.; McGovern, E.S.
submitted to the EMBL Data Library, July 1992
A; Description: A transforming gene isolated by expression cloning from Ewing's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P41279; Experimental source: TCO-4 cells ; Experimental source: TCO-4 cells ; Note: sequence inconsistent with nucleotide translation ; Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBIP:138971)
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12.8%; Score 74; DB 2; Length 824;
Best Local Similarity 29.3%; Pred. No. 10;
Matches 29; Conservative 13; Mismatches 31; Indels
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A;Molecule type: mRNA
A;Residues: 1-467 <CHA>
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Cross-references: UNIPROT:P12580; EMBL:U36624; NID:g1276642; PIDN:AAB68158.1; PID:g103; Steplen, P.P.; Margossian, S.P.; Landsman, D.; Butow, R.A.
coc. Natl. Acad. Sci. U.S.A. 89, 6813-6817, 1992
Title: The yeast nuclear gene suv3 affecting mitochondrial post-transcriptional proces; Reference number: A46190; WUID:92357722; PMID:1379722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: sequence extracted from NCBI backbone (NCBIP:111103)
Stepien, P.P.; Margossian, S.P.; Landsman, D.; Butow, R.A.
Ubmitted to the EMBL Data Library, April 1992
Description: The yeast nuclear gene suv3 affecting mitochondrial post-transcriptional
Reference number: S27462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable RNA helicase SUV3, ATP-dependent, precursor - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein LPB2w; protein YPL029w
CiSpecies: Saccharomyces cerevisiae
CiDate: 16-May-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004
CiAccession: $63453; A46190; $27462
CiAccession: $63453; A46190; $27462
Submitted to the EMBL Date Library, September 1995
A;Reference number: $63452
                                                                                                                                                                                                                                                                                          1-164,'R',166-597,'DL',600-615,'A',617-636,'D',638-663,'D',665-737
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                                                                                                                                                                                                                                                 41 MKKLSDLEAQWAPSPRLQAQSLLPAVCHHPAL - - PQDLQPVCASQEASSIFKTLRTIAND
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Cross-references: EMBL:M91167; NID:9172797; PIDN:AAA35135.1; PID:9172798
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F;1-25/Domain: transit peptide (mitochondrion) #status predicted cTNP>
F;26-737/Product: probable RNA helicase #status predicted cMAT>
F;239-246/Region: nucleotide-binding motif A (P-loop)
F;320-325/Region: nucleotide-binding motif B
F;324-327/Region: DEAD/H motif #status atypical
                                                                                                                                                                             10,
                                                                                                         Length 467;
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                                                                                                         DB 2;
C; Keywords: alternative initiators; proto-oncogene F; 136-388/Domain: protein kinase homology <KIN>
                                                                                                 Query Match
12.4%; Score 72; DB 2
Best Local Similarity 32.0%; Pred. No. 9;
Matches 24; Conservative 16; Mismatches
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R.K.; Vo

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132 KTYVPSVSEIIHPSSPGNL 150
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Species: Yersinia pestis
C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0386
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.;
I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 AKUR.
A;Residues: 1-369 AKUR.
A;Cross-references: UNIPROT:Q8ZC40; GB:AL590842; PIDN:CAC92418.1; PID:g15981121; GSPDB:C
C;Genetics:
A;Gene: ribb
C;Superfamily: Chlamydophila pneumoniae riboflavin-specific deaminase
C;Keywords: oxidoreductase
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Query Match
11.8%; Score 68.5; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 16;
Matches 27; Conservative 16; Mismatches 32; Indels 31; Gaps

12 GVAVVLLLLLQSTQSY-----YIQYQGFRVQLESMKKLSDLEAQWAPSPRLQ 58 59 AQSLLPAVCHHPALPQDLQPVCASQEASSIFKTLRTIANDDCELCV 104 179 ઠ g ð 셤

Search completed: March 26, 2005, 16:49:40 Job time : 23.708 secs

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                                                                                                                                                     March 26, 2005, 16:51:20 ; Search time 71.0357 Seconds
(without alignments)
129.758 Million cell updates/sec
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P01559
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Q47185
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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Q8VUT3

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Q7TWR1

Q9CCV9

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Q8CCM2

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Gapop 60.0 , Gapext 60.0
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Q8PNN9
Q8CBH7
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1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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18
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Match Length DB
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1210
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Perfect score:
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                                                                                                     OM protein
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Q83bf3 coxiella bu	Q83a72 coxiella bu	Q96jp7 homo sapien	O9stc3 elaeis guin	022376 oryza sativ	Q6at12 oryza sativ		Q6c751 yarrowia li	-	Q83an4 coxiella bu	Q83f74 coxiella bu	Q8z370 salmonella	O82232 arabidopsis	Q83aq6 coxiella bu
Q83BF3	Q83A72	Q96JP7	Q9STC3	022376	Q6ATL2	Q62MM8	Q6C751	Q688G0	Q83AN4	Q83F74	Q8Z370	RC22 ARATH	Q83A <u>Q</u> 6
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32	33	34	35	36	37	38	39	40	41	42	43	44	45

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guanylate
intestinal
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                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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                                                                                                                                                                                                                           STRAIN=042: K86:H37 / 18D / ETEC;
MEDLINE=81264141; PubMed=7021541;
Chan S.-K., Giannella R.A.;
"Amino acid sequence of heat-stable enterotoxin produced by Bscherichia coli pathogenic for man.";
J. Biol. Chem. 256:7744-7746(1981).
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 1.9e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      9 17
18 AA; 1978 MW; D0C975F49D600650 CRC64;
               01, Created)
01, Last sequence update)
44, Last annotation update)
18 AA
                                05-JUL-2004 (Rel. 44, Last annotati
Heat-stable enterotoxin ST-2 (ST-B)
Escherichia coli.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                        1 NTFYCCELCCYPACAGCN 18
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative C
STANDARD;
                21-JUL-1986
21-JUL-1986
HSTB ECOLI
P01560;
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RESULT 2

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P55936 Q86rb2 Q83ak0

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Dallas W.S.;
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              RESULT 4
HST1_ECOLI
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PubMed=1536495;
Reischl U., Youssef M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
Real-time fluorescence PCR assays for detection and characterization of heat-labile I and heat-stable I enterotoxin genes from of heat-labile I she heat-stable I enterotoxin genes from of heat-labile I and heat-stable I enterotoxin genes from of Scherichia coli.";
J. Clin. Microbiol. 42:4092-4100(2004).
EMBL; AY342057; AAQ22974.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                   MEDLINE=89108617; PubMed=2912902; Mediatino A., Giannella R., Thompson M.R.; Potrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical to the 18-amino-acid Escherichia coli heat-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%; Score 10; DB 2; Length 18; 100.0%; Pred. No. 7.2e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          PFam; PF02048; Enteroctoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AA; 6927 MW; 646D4AE2F899D957 CRC64;
                          01-WAR-2004 (TrEMBLrel. 26, Created)
1-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Heat-stable enterotoxin ST-Ia.
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Heat-stable enterotoxin ST-Ia (Fragment).
18
                                                                                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001489; Enterotoxin HS.
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PRT;
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                                                                                                                                                                                                                                                stable enterotoxin (ST Ia).";
Infect. Immun. 57:649-652(1989).
PIR; A60103; A60103.
HSSP; P01559; IETN.
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Best Local Similarity 100.
Marches 10; Conservative
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es 10; Conservative
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PRELIMINARY;
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                                                                                           freundii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                       NCBI_TaxID=546;
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                                                                                           Citrobacter
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SEQUENCE
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Q7M0U3
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44 NTFYCCELCC 53

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crystallography of weakly toxic and nontoxic analogs.";
Biochemistry 33:8641-8650(1994).
-!- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5; Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.; "Mode of disulfide bond formation of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli."; PEBS Lett. 215:165-170(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=8249571; PubMed=2990268; Sekizaki T., Akashi H., Terakado N.; Sekizaki T., Akashi H., Terakado N.; "Nuclocida sequences of the genes for Escherichia coli heat-stable enterctoxin I of bovin, avian, and porcine origins."; Am. J. Vet. Res. 46:909-912(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okamoto K., Takahara M.;
"Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94312375; PubMed=8038153; Sato T., Cataube Y., Shimonishi Y.; Sato T., Ozaki H., Hate Y., Kitagawa Y., Kateube Y., Shimonishi Y.; Structural characteristics for biological activity of heat-stable enterotoxin produced by enterotoxigenic Escherichia coli: X-ray
                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                        SO M., McCarthy B.J.;
"Nucleotide sequence of the bacterial transposon Th1681 encoding alear-stable (ST) toxin and its identification in enterotoxigenic Escherichia coli strains.";
Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SÜBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the heat-stable enterotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ne heat-stable toxin I gene from Escherichia coli 18D.";
Bacteriol. 172:5490-5493(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pro form and role of the pro sequence in secretion.";
J. Bacteriol. 172:5260-5265(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
Heat-stable enterotoxin ST-IA/ST-P precursor.
72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-042:K86:H37 / 18D / ETEC;
MEDLINE-90368614; PubMed-2203756;
                                                                                                                                                                                                                                                                      TRANSPOSON=Tn1681;
MEDLINE=81054703; PubMed=6254008;
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                               Escherichia coli.
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MEDIJINE=89108616; PubMed=2643580;
Guzman-Verduzio L.M., Kupersztoch Y.M.;
Guzman-Verduzio L.M., Kupersztoch Y.M.;
"Rectification of two Escherichia coli heat-stable enterotoxin allele sequences and lack of biological effect of changing the carboxy-terminal tyrosine to histidine.";
Infect. Immun. 57:645-648(1989).
-!- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal
                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15364995;

Rejechl U., Yousee M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
Rejechl U., Yousee M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
"Real-time fluorescence PCR assays for detection and characterization of heat-labile I and heat-stable I enterotoxin genes from enterotoxigenic Escherichia coli.";
J. Clin. Microbiol. 22:4092-4100(12004).

EMBL; AY342058; AQ92975.1;
GQ; GO:0005976; C:extracellular; IEA.
GQ; GO:0005405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 1 1 1 SEQUENCE 61 Aa; 6658 MW; 1D75955D7AF0DED2 CRC64;
                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Heat-stable enterotoxin ST Ib (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.9%; Score 7; DB 2;
100.0%; Pred. No. 0.65;
tive 0; Mismatches
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15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin A2 precursor (STA2).
                                                                61 AA
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PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
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                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Escherichia coli
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ID HST2 ECOLI
AC Q47185;
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"Real-time fluorescence PCR assays for detection and characterization of heat-labile I and heat-stable I enterotoxin genes from enterotoxigenic Escherichia coli.";
U.C.In. Microbiol. 42:4092-4100(2004).
BMBL; AY342059; AA092976-11;
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
HITHERPROISE: BRECTOXIN_HS.
PROSITE; PS000273; ENTEROTOXIN_H STABLE; 1.
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                PDB; 1ETL; X-ray; @=59-71.
PDB; 1ETN; X-ray; @=-
PDB; 1ETN; X-ray; @=-
InterPro; IFRO1489; Enterotoxin_HS.
Pf02048; Enterotoxin_HS; 1.
PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.
3D-Structure; Enterotoxin; Signal; Toxin; Transposable element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8075 MW; 92E8B766B3988264 CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Heat-stable enterotoxin ST Ib (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 7; DB 2;
100.0%; Pred. No. 0.65;
tive 0; Mismatches
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or send an email to license@isb-sib.ch)
                                                    EMBL; V00612; CAA23883.1; -. EMBL; M58746; AAA62776.1; -. EMBL; M25607; AAA24653.1; -. PIR; A01822; QHEC1.
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Best Local Similarity 100.
Matches 10, Conservative
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Matches 7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                     evidence of extracellular processing.";
Mol. Microbiol. 4:265-273 (1990)
-!- FUNCTION: Toxin which activates the particulate form of guanylate
cyclase and increases cyclic GMP levels within the host intestinal
                  gene encoding the heat-stable toxin
                                                                                                                                                                                                                  MEDLINE-87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5; Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Almoto S., Takeda T., Miwatani T., Takeda Y.; "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
                                                                                                                                         "Amino-acid sequence of a heat-stable enterotoxin produced by human enterotoxigenic Escherichia coli.";
Eur. J. Biochem. 129:257-263 (1982).
                                                                                                                                                                                                                                                                                                                                                        Rasheed J.K., Guzman-Verduzco L.M., Kupersztoch Y.M.; "Two precursors of the heat-stable enterotoxin of Escherichia coli:
                                                                                                   Almoto S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y., Miwatani T.:
                                                                                                                                                                                                                                                                            produced by a human strain of enterotoxigenic Escherichia coli."; REBS Lett. 215:165-170(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SÜBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat-stable enterotoxin A3/A4.
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PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
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"Cloning and hyperexpression of a Gene at a colin,"
                                                                                              MEDLINE=83105138; PubMed=6759126;
                                                                                                                                                                                                                                                                                                                                          MEDLINE=90251166; PubMed=2187146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03311; AAA24652.1; --
EMBL; M34345; AAA2390.1; --
EMBL; M18446; AAA2330.1; --
EMBL; M29255; AAA24686.1; --
EMBL; M29255; AAA24686.1; --
PIR; J70373; QHECIB.
HSSP; P01559; 1ETV.
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                                                  Gene 81:219-226(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelial cells.
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SEQUENCE OF 54-72.
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Best Local Similarity
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63
19
72 AA;
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Q85824
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Moseley S.L., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
"Isolation and nucleotide sequence determination of a gene encoding a
heat-stable enterotoxin of Escherichia coli.";
Infect. Immun. 39:1167-1174(1983).
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MEDDLINE-89108616; PubMed=2641580;
Guzman-Verduzio L.M., Kupersztoch Y.M.;
Guzman-Verduzio L.M., Kupersztoch Z.M.;
"Rectification of two Escherichia coli heat-stable enterotoxin allele sequences and lack of biological effect of changing the carboxy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ō
                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;
Dwarakanath P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L., Bolivar F., Kupersztoch Y.M.; "Cloning, sequencing, and expression in Ficoll-generated minicells of an Bacherichia coli heat-stable enterotoxin gene."; Plasmid 20:42-53(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L;
Zhou X., Shen L.P., Chi C.W.;

"Isolation and nucleotide sequence determination of a gene encoding heat-stable enterotoxin of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                   HST3 ECOLI STANDARD; PRT; /2 AA.
010955; PSE588;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-IB) (ST-H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                 Length 72;
                                                                                                                                                           Heat-stable enterotoxin A2
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By similarity.
By similarity.
D87850306E06E260 CRC64;
                                                                                                                                                                                                                                                   DB 1;
o. 0.73;
                               PIR; JS0292; QHECIB.
HSSP; P01559; 1ETN.
INTERPO; IPR001489; ENTEROTOXIN HS.
PFam; PF02048; ENTEROTOXIN HS; 1.
PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
                                                                                                                                                                                                                                                 38.9%; Score 7; DB 1
100.0%; Pred. No. 0.7
ive 0; Mismatches
                                                                                                                                            By similarity
                                                                                                                            Potential
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Infect. Immun. 57:645-648(1989).
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MEDLINE-89202548; PubMed=3071819;
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                                                                                                                                                                                                                   7895 MW;
                    EMBL; M18345; AAA23729.1;
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72
64
68
                                                                                                             Enterotoxin; Signal; SiGNAL 1
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les 7; Conserv
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HSTA YEREN P07593;
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| Drahim A., Liesack W., Stackebrandt E.;

Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
                                                                                                                           DOI=10.1128/JB.185.17.5320-5323.2003;
Gregory M.A., Till R., Smith M.C.M.;
"Integration Site for Strepponyces Phage {phi}BT1 and Development of Site-Specific Integrating Vectors.";
J. Bacteriol. 185:5320-5323(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                            Bacteriophages.";
Thesis (2000), Department of Genetics, University of Nottingham, Nottingham, Nottingham, ONITED KINGDOM.
                                                                RNA stage; Caudovirales; Siphoviridae;
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Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                 "Characterisation and Evolution of Homoimmune Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                     Length 120;
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                                                                                                                                                                                                                                                                                          Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases EMBL; AJ550940; CAD80131.1; -. GO; GO:0004519; F:endonuclease activity; IEA. GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                        507; HNHC; 1.
120 AA; 13827 MW; 2EAEC16389699723 CRC64;
          I-JUN-2003 (TrEMBLrel. 24, Created)
I-JUN-2003 (TrEMBLrel. 24, Last sequence update)
I-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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(Rel. 26, Last sequence update)
(Rel. 44, Last annotation update)
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                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22803275; PubMed=12923110;
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                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002711; HNH.
InterPro; IPR003615; HNH nuc.
Pfam; PP01844; HNH; 1.
SMART; SM00507; HNHc; 1.
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                                                                Viruses; dsDNA viruses,
Lambda-like viruses.
NCBI _TaxID=225588;
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Yersinia kristensenii.
                                                      Bacteriophage phi-BT1
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Best Local Similarity
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                                                                                                                                                                                                        Gregory M.A.;
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P31518;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eur. J. Blochem. 152:199-206 (1985).
-!- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding
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-1- SUBCELLULAR LOCATION: Secreted.
-1- INDUCTION: In cultured cells, expressed only at temperatures <10
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STRAIN=Serctype O:8;
MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
Lichalim A., Liceack W., Pike S., Stackebrandt E.;
"The polymerase chain reaction: an epidemiological tool to differentiate between two clusters of pathogenic Yersinia entercoolitica strains."
FEMS Microbiol. Lett. 76:63-66(1992).
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Takao T., Tominaga N., Yoshimura S., Shimonishi Y., Hara S., Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 66
                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
By similarity.
By similarity.
27BE7006675CC075 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 11, Mismatches
                                                                                                                                                                                             HSSP, P01559; 1ETN.
Intearro; IPRO01489; Enterotoxin HS.
Pfam; PP02048; Enterotoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN H_STABLE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogenic and nonpathogenic yersiniae.";
Infect. Immun. 58:2983-2988(1990).
                                                                                                                                                                                                                                                                                                                                     Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae, Yersinia.
                                                                                                                                       EMBL; X69218; CAA49152.1; -. PIR; S31652; S31652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=W1024 / Serotype 0:9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ystA; Synonyms=yst;
Yersinia enterocolitica.
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                                                                                                                                                                                                                                                                                                         Enterotoxin; Signal SIGNAL 1
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54
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58
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EMBL; D63578; BAA23656.1; -.
                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia enterocolitica
                                                                                                                                                                                            52
71
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68
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    12 PACAGC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSTC YEREN
050319;
                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                            PROPEP
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HSTC_YEREN
                                                                                                                                                                                                              CHAIN
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degrees Celsius. Under conditions of high osmolarity and alkaline pH (as it is the case in the host's intestine), it is expressed at 37 degrees Celsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=84-50 / Serotype 0:5;
MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel B.,
Maruyama T., Fukushima H., Takeda T.;
"The novel heat-stable enterotoxin subtype gene (ystB) of Yersinia enterocolitica: nucleotide sequence and distribution of the yst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                          SIMILARITY: Belongs to the heat-stable enterotoxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat-stable enterotoxin A.
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001489; Enterotoxin_HS.
Pfam; PF022048; Enterotoxin_HS, 1.
PROSITE; PS033; BNTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
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022F99B3800C861B CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UL-2004 (Rel. 44, Last annotation update)
Heat-stable enterotoxin B precursor (Y-STB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 11; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6;
                                                                                                                                                                                                                                                   EMBL; X65999; CAA46801.1; -. EMBL; U09235; AAA18472.1; -. PIR; S25659; S25659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%;
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71
71
71
78
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wes 6; Conserv
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P74977;
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DISULFID
DISULFID
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Matches
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HSTB YEREN
HSTB YEREN
HSTB YEREN
HSTB YEREN
DT 15-DE
DT 15-DE
DT 05-JU
DB Heat-
DB Heat-
DB Heat-
CC Bacte
OC Bacte
OC Bacte
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CC STAAL
RY MEDLI
RY GENEE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"Nucleotide sequence of a gene encoding the novel Yersinia
entercocolitica heat-stable enterctoxin that includes a pro-region-like
sequence in its mature toxin molecule.";
Microb. Pathog. 22:89-97(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a highly toxic, large molecular size heat-stable enterotoxin produced by a clinical isolate of Yersinia enterocolitica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=Serctype O:3;
MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
YOSHINO K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
Shimonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 71;
                                                                                                                                                   InterPro; IPR001489; Enterotoxin HS.
Pfam; PF02048; Enterotoxin HS; 1.
PR0SITE; PS00273; ENTEROTOXIN H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19 Potential.
                                                                                                                                                                                                                                                                                                                                      Heat-stable enterotoxin
                                                                                                                                                                                                                                                                                                                                                                     By similarity.
By similarity.
By similarity.
ED6E9F61ACDD4F50 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1920 (Rel. 34, Last annotation update)
Heat-stable enterotoxin C precursor (Y-STC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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100.0%; Pred. No. 11;
-ive 0; Mismatches
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                                                                                              EMBL; D88145; BAA13544.1; -. HSSP; P01559; 1ETN.
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Search completed: March 26, 2005, 17:24:51
Job time : 72.0357 secs
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Matches
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Strl converting bacteriophage.
Strl sonverting viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBI_TaxID=194948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
STRAIN=0157:H7 / EDL935 / ATCC 700927 / EHEC;
MEDLINE=2107-935; PubMed=11206551; DOI=10.1039/35054089;
Perna N.T., Plunkert G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharana T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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InterPro; IPR001489; Enterotoxin_HS.
Pfam; PP02048; Enterotoxin_HS; 1.
PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL
                                                                                                                                                        Heat-stable enterotoxin C
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                                                                                                                                                                                By similarity.
By similarity.
By similarity.
7C0D83893C2F981D CRC64;
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1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Putative lysis protein S of prophage CP-933V.
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Last annotation update)
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100.0%; Pred. No. 13;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                        h 33.3%; Score 6; DB 1 Similarity 100.0%; Pred. No. 11; 6; Conservative 0; Mismatches
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                           7639 MW;
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Complete proteome.
SEQUENCE 90 AA; 10060 M
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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01-OCT-2003 (
01-OCT-2003 (
                                                                                                                                                                          DISULFID
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                                                                                                                                                        CHAIN
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Q8X4M8
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                                                                                                         DOI=10.1128/JB.185.13.3966-3971.2003;
Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T., Takeda Y., Yamasaki S.; Hamabata T., Takeda Y., Takeda Y., Satolone analysis of a novel Shiga toxin 1 (Stx1)-converting phages but not to other Stx1-converting phages.;
J. Bacteriol, 185:3966-3971(2003).

EMBL, APOS153; BAC77969.1;
InterPro; IRP007054; Lysis_S.

Pfam; PF04971; Lysis S; I.

SEQUENCE 96 AA; 10684 MW; CF1562C30DA56B19 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%; Score 6; DB 2;
100.0%; Pred. No. 14;
tive 0; Mismatches
[1]
SEQUENCE FROM N.A.
STRAINESEX1 phage;
MEDLINE=22697399; PubMed=12813092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 FYCCEL 18
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ST Ib rec ST recept Amino aci ST Ib rec ST recept

Immature Sequence . coli

ST recept Amino aci Escherich

Aar20352 Aar71975 Aar85971 Aay40533 Adr485876 Aay40538 Adr48652 Aay40538 Aar85970 Aay40534 Aar85970 Aay40534 Aar85970 Aay40534 Aar85973 Aay40535

ST Ib recept Amino aci ST Ib rec ST recept Amino aci ST Ib rec

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ALIGNMENTS
             AAR71975
ADR48356
ADR48356
ADR48356
ADR48596
ADR485970
ADR85972
ADR85977
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                                                                                               AAY40535
AAR85948
March 26, 2005, 16:49:45; Search time 84.4821 Seconds (without alignments) 86.982 Million cell updates/sec
                                                                                                              2105692
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                         2105692 segs, 386760381 residues
                        sw model
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                                                                NSSNYCCELCCNPACNGCY 19
                        protein search, using
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Maximum DB seq length: 2000000000
                                                     US-10-775-481A-5
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Scoring table:

score:

Title: Perfect

Sequence:

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Word size :

Searched:

A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
5: geneseqp2001s:*
5: geneseqp2003s:*
7: geneseqp203bs:* geneseqp2004s:*

Post-processing: Listing first 45 summaries

Database :

receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;

94WO-US012232.

26-OCT-1994;

26-OCT-1993;

ST Ib receptor ligand portion.

19-JAN-1996

AAR85948;

colorectal, metastasis.

Escherichia coli.

WO9511694-A1

04-MAY-1995.

AAR85948 standard; peptide; 19 AA.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aar85948 ST ib rec	Aay40510 ST recept	5 Ami	Aar85970 ST Ib rec	Aay40532 ST recept	Adr45846 Amino aci	Aar95923 Enterotox		~	Aay06972 E. coli h	Aay02398 Heat stab		Aaol6204 E coli sm	Abg74825 E. coli h	0	Adc14123 Modified	Adc14121 Modified	Adr48340 Bacterial	Adr48360 Analgesic	Adr48359 Analgesic	8	Adr48329 E. coli S	Adr48404 GC-C acti	Adr48372 Analgesic	Adr48413 GC-C acti
SUMMARIES	ID		AAY40510	ADR45825	AAR85970	AAY40532	ADR45846	AAR95923	AAY02386	AAY29608	AAY06972	AAY02398	AAM51879	AA016204	ABG74825	ADC14120	ADC14123	ADC14121	ADR48340	ADR48360	ADR48359	ADR48398	ADR48329	ADR48404	ADR48372	ADR48413
	03	7	~	œ	7	~	œ	~	~	7	7	7	4	9	9	7	7	7	8	æ	œ	æ	80	80	80	8
	Length	19	1.9	19	18	18	18	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	21	21
و عله	Match	100.0	100.0	100.0	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9	78.9
	Score	19	19	19	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
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New conjugated compounds are provided which consist of (1) an ST receptor binding molety and (2) an active molety which is a radio- stable agent. ST' refers to a heat stable toxin produced by E.coli and other corganisms. Bspecially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tummours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate Conjugated cpds. which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent. Claim 3; Page 116; 133pp; English. (UYJE-) UNIV JEFFERSON THOMAS 93US-00141892. 94US-00305056. WPI; 1995-178646/23. Sequence 19 AA; 13-SEP-1994; Waldman SA; 

100.0%;

19; Conservative

Similarity

Query Match Best Local S Matches 19

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The specification describes a method for increasing the number of heat stable toxin (ST) receptor molecules on the surface of a metastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the number of ST receptor molecules on the surface of the cancer cell is increased. Therapeutic compositions comprising components which target ST receptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that have diseases that affect colorectal, gastric and oesophageal cells, including colorectal, gastric can desphageal cells, including colorectal, gastric can be supposed and cells including colorectal, gastric can be supposed cells including colorectal, gastric can be supposed cells. Including colorectal, gastric can be supposed cells including colorectal, gastric can be supposed cells. Including colorectal can be supposed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.
                          heat stable toxin, ST, ST receptor; colorectal cancer; gastric cancer; oesophageal cancer; colorectal cell; gastric cell; oesophageal cell; ST Ib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
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100.0%; Pred. No. 9.5e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Schulz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID NO 5; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR85970 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Park J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSSNYCCELCCNPACNGCY 19
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                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ST Ib receptor ligand portion.
                                                                                                                                                                                                                                                                                    .0-FEB-2004; 2004WO-US003765.
                                                                                                                                                                                                                                                                                                                                  10-FEB-2003; 2003US-0446730P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pitari GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADR45824
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                                                                                                                                                                              WO2004071436-A2.
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                                                                                                                               Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells. The present sequence represents the amino acid sequence of a ST receptor peptide ST 1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (heat-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stable toxin) receptor moiety selected from one of the sequences shown i AAV40508-Y40559 and an active moiety (antisense molecule). The compound
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugated compound comprising a receptor moiety and active moiety, useful for the treatment/prevention of colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to a conjugated compound that comprises a ST
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0
                            Length 19;
Score 19; DB 2; Lengtu 1., Pred. No. 9.5e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of heat stable toxin ST Ib.
                                                                                                                                                                                                                                                                                              AAY40510 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 21-22; 23pp; English.
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(UYJE-) UNIV JEFFERSON THOMAS

26-OCT-1993; 36-JUN-1995;

WPI; 1999-571264/48. N-PSDB; AAZ07541.

Waldman SA;

95US-00467920. 93US-00141892.

(first entry)

03-DEC-1999

AAY40510;

receptor peptide ST 1b

Escherichia coli.

US5962220-A 05-OCT-1999 ö

Gaps

ADR45825 standard; peptide; 19

18-NOV-2004 (first entry)

ADR45825;

RESULT 3
ADR45825
ID ADR4
XX
AC ADR4
XX
DT 18-N
XX
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1 NSSNYCCELCCNPACNGCY

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Sequence 19 AA;

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AAY40508-Y40559 and an active moiety (antisense molecule). The compound
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                                                                  Query Match
                                                                                      Matches
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                                                                                                                                                                New conjugated compounds are provided which consist of (1) an ST receptor binding molety and (2) an active molety which is a radio- stable agent. 'ST' refers to a heat stable toxin produced by B.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a conjugated compound that comprises a ST (heatstable toxin) receptor moiety selected from one of the sequences shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ST receptor; heat-stable; toxin; colorectal cancer.
                                                                                                       Conjugated cpds, which specifically bind to colorectal cancer cells comprise heat-stable toxin receptor binding moiety and active moiety which may be a therapeutic agent or a radioactive agent.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and active moiety,
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                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                     Score 15; DB 2; Le
Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                               Claim 3; Page 120; 133pp; English
                                                                                                                                                                                                                                                                             78.9%; Sc.__
100.0%; Pre
0; 1
                                                                                                                                                                                                                                                                                                                                                                                                AAY40532 standard; peptide; 18 AA
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                                               (UYJE-) UNIV JEFFERSON THOMAS
                   93US-00141892.
94WO-US012232
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                                                                                                                                                                                                                                                                                                                             12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugated compound;
                                                                                      WPI; 1995-178646/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                   Sequence 18 AA;
26-OCT-1994;
                           13-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1993;
                  26-OCT-1993;
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                                                                 Waldman SA;
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is useful for the treatment of colorectal cancer. The use of the conjugated compound is advantageous compared to antibodies since it binds specifically to colorectal cells and has no toxic effect on normal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oesophageal cells, including colorectal, gastric or oesophageal cancers. The present sequence represents a fragment of a ST designated ST Ib (see ADR45825), which is used as the ST receptor ligand in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin; ST; ST receptor; colorectal cancer; gastric cancer; cancer; colorectal cell; gastric cell; oesophageal cell;
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                          Length 18;
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                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of heat stable toxin ST Ib fragment.
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                                                                                                                                                                          DB 2; Le
2.1e-09;
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                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                             Score 15;
Pred. No.
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                                                                                                                                                  78.9%; Scc...
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR45846 standard; peptide; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2004; 2004WO-US003765.
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nes 15; Conserv
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Best Local Similarity
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oesophageal c
ST Ib.
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The specification describes a method for selecting a candidate drug compound having affinity for biological receptors. The method uses a combination of rational and combinatorial drug design techniques. At least 1 residue in the original cell receptor binding peptide is modified to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method its used for identification of a candidate receptor antagonist or agonist. The present peptide is a cell receptor binding peptide, and can thus be used as a starting point for identification of candidate drug compounds, using the method of the invention
                        Selection; candidate drug; cell receptor binding; affinity;
biological receptor; rational drug design; combinatorial drug design;
receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
                                                                                                                                                                                                                                                                                                                                                       Method of drug selection - and use of an acetamidomethyl-protected polymer as a substrate in the solid state synthesis of an oligopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat stable ST enterotoxin; immunoreagent; radiological therapy; diagnosis; ST receptor binding moiety; macrocyclic complexing agent; tumour; infectious diarrhoeal disease; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 15; DB 2; Length 19; 100.0%; Pred. No. 2.2e-09; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 1-2; 38pp; English.
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100.08; Pit
Heat stable ST enterotoxin Sth.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                   Escherichia coli
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                                                                                                                                                                                             20-AUG-1998;
                                                                                                                                 WO9909416-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mucosal binding compositions for generating mucosal immune response - comprises mucosal binding peptide, pref. derived from cholera toxin, and an antigen, e.g. derived from E. coli, HIV, etc.
 Gaps
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                                                                                                                                                                                                                                                   Mucosal binding composition; mucosal binding polypeptide; antigen; non-viral pathogen; sexually transmitted disease; administration; voginal; rectal; oral; immune response; secretory immunity; mucous; enterotoxigenic; STa protein.
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Pred. No. 2.2e-09;
0; Mismatches 0;
                                                                                                                                                                                                                        Enterotoxigenic E. coli STa protein antigen.
Mismatches
                                                                                                                                  AAR95923 standard; peptide; 19 AA.
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100.0%; Pr
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                           1 NSSNYCCELCCNPAC 15
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                                               1 NSSNYCCELCCNPAC
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LEBE/) LEBENS M R. (HOLM/) HOLMGREN J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-268614/27.
                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                          WO9616178-A1
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Matches
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AAY02386
ID AAY02
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AC AAY0
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Gaps

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99WO-GB000396.

08-FEB-1999;

(first entry)

09-JUL-1999

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The invention provides a targeting immunoreagent that comprises a metal ion and an immunoreactive group covalently bonded to a terpyridine complexing agent of a specified formula. The immunoreagent is useful in diagnostic imaging and therapeutic compositions. The immunoreagent is used for radiological treatment of tumours. When the immunoreagent contains yttrium, the radiation toxicity is lower compared with other yttrium chelators. The immunoreagent is not rapidly metabolized and does not disperse and efficiently forms covalent bonds with proteins and other biological molecules. The immunoreagent has good emission characteristics and are easily spectrophotometrically analysed. Protein conjugates can be stored for metal complexing without activation steps that degrade protein. The terpyridine complexing agent rapidly complex with metals and the obtained chelates have good tabbility. Sequences AAY06971-976 represent examples of heat stable ST enterotoxin peptides that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used as the immunoreactive group in the immunoreagent of the invention
                                                               Targeting immunoreagent for diagnostic imaging and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%; Scc.
100.0%; Pre
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                                                                                                                            Claim 16; Page 50; 57pp; English.
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                        WPI; 1999-302905/25.
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                                                                                       compositions
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                       radiological therapy of tumours. In addition, a variety of bacteria, including Escherichia coli, Vibrio cholerae, Citrobacter freundii, and versinia enterocollitos, bind to ST receptors and cause infectious diarrhoeal diseases, particularly in pediatrics and in developing countries. These types of diarrhoea can also be treated using TI's. TI's may specifically used to treat cancers and also be used as an antidiarrhoeal agent. TI's are free from the various disadvantages of prior art reagents, including rapid destruction and/or excretion, instability in storage, and protein degradation. There is no perturbation of protein reactive groups at the pyridyl chelating site. AAY29607 to AAX29612 represent examples of heat stable ST enterotoxins given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                         The present invention describes targeting immunoreagents (T1's) comprising a metal ion and a residue of a macrocyclic complexing agent (MCA). T1's are of use in diagnostic imaging and therapy of specific disease sites in a patient, using either radioactive, magnetic resonance, or fluorescent means of detection or use of the metal ion; alternatively, a substituent of these types may be introduced, e.g. radioactive iodine, to perform the same function. Most notable is the imaging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Targeting immunoreagent, metal ion; immunoreactive; terpyridine; tumour; complexing agent; diagnostic imaging; radiological treatment; yttrium; therapeutic; radiation toxicity; heat stable; ST enterotoxin.
                                                                                                                                                                                       Macrocyclic complexing agents containing linked 2,6-pyridinylene nuclei as components of targeting immunoreagents binding to ST receptor.
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; Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli heat stable ST enterotoxin peptide Sth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                      Black C,
                                                                                                                                                                                                                                                    Disclosure; Page 39; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.9%; Scc...
100.0%; Pre
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                                                                                                      Shah C,
  98US-00020233
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                                       (NYCO-) NYCOMED IMAGING AS. (MATT/) MATTHEWS D P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NYCO-) NYCOMED IMAGING AS. (MATT/) MATTHEWS D P.
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                                                                                                    Snow RA, Delecki DJ,
                                                                                                                                             WPI; 1999-494219/41.
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06-FEB-1998;
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Matches

RESULT 10

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Gaps

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Length 19; 0; Indels

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Mismatches

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Selection; candidate drug; cell receptor binding; affinity; biological receptor; rational drug design; combinatorial drug design; receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic; gamma-turn mimetic; bata sheet mimetic; disulphide bridge mimetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method of drug selection - using a combination of rational and combinatorial drug design techniques.
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Guanylate cyclase receptor agonist; apoptosis induction; cancer; polyps; inflammation; asthma; nephritis; heparitis; brondhitis; cystic fibrosis; small heat stable enterotoxin tricyclo; inflammatory bowel disease; pancreatitis; ulcerative collitis; Crohn's disease; Kaposi's sarcoma.

Location/Qualifiers

Escherichia coli

6. .10

Disulfide-bond Disulfide-bond Disulfide-bond

E coli small heat stable enterotoxin tricyclo peptide, SEQ ID No 23.

(first entry)

28-MAR-2003

AA016204;

AA016204 standard; peptide; 19 AA.

RESULT 13 AA016204

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compound having affinity for biological receptors. The method uses a combination of rational and combinatorial drug design techniques. At least 1 residue in the original cell receptor binding peptide is modified to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method is used for identification of a candidate receptor antagonist or agonist. The present peptide is a cell receptor binding peptide, and can thus be used as a starting point for identification of candidate drug compounds, using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compound for detecting and treating metastatic colorectal cancer comprises a conjugate of an STa peptide and an immunogenic protein which binds to the guanyl cyclase-c receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a conjugate which comprises an E. coli thermostable enterotoxin (STa) peptide and an active molecule where the STa peptide has a conformation such that it is capable of binding to the guanyl cyclase-C (GC-C) receptor. This can be used in the specific diagnosis and treatment of metastatic colorectal cancer. The present sequence is a fragment of the human thermostable enterotoxin (STh)
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cyclase-C; GC-C; STa.
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100.0%; Pred. No. ...
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel guanylate cyclase receptor agonist peptide useful for preventing treating primary or metastatic cancer and polyps in a patient, and for inducing apoptosis in the cells of a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 47pp; English.
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100.0\frac{\pi}{8}; \text{Fig.} \text{Vi.}
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                                                                                                                                                                                                                                                                                                                                             ; 2001US-0279438P.
; 2001US-0300850P.
; 2001US-0303806P.
; 2001US-0307358P.
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29-MAR-2001; 2001US-0279438P.
27-JUN-2001; 2001US-0300850P.
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17-JAN-2002; 2002US-0348646P
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NSSNYCCELCCNPAC 15

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Apical membrane; mucosal epithelial cell; respiratory tract; guanylate cyclase C; G protein-coupled receptor; guanosine triphophate; cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation; membrane-associated type II protein kinase; mucus fluidisation; cystic fibrosis transmembrane conductance regulator; breathing disorder; mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma; chronic bronchils; cystic fibrosis; enterotoxin; heat stable.
                                                                                                                                                                                                                                                                                                                                      Composition useful for treating respiratory disease, comprises a peptide that activates guanylate cyclase C, and is delivered to the apical membrane through the respiratory tract.
                                         B. coli heat stable enterotoxin derived peptide SEQ ID 7.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 4; 23pp; German.
                                                                                                                                                                                                                  05-JUN-2002; 2002WO-DE002040.
                                                                                                                                                                                                                                         05-JUN-2001; 2001DE-01027119.
                     (first entry)
                                                                                                                                                                                                                                                                                                                 WPI; 2003-156842/15.
                                                                                                                                                                                                                                                                                            Cetin Y, Savas Y;
                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                            (CETI/) CETIN Y. (SAVA/) SAVAS Y.
                                                                                                                                                                        WO200298912-A2
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                      12-JUN-2003
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 ABG74825;
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This invention describes a novel medicament in a formulation that is delivered to the apical membrane of mucosal epithelial cells through the cespitactory tract. The medicament contains at least one peptide that activates guanylate cyclase (GCC). GCC is a G protein-coupled receptor that catalyses conversion of guanosine triphophate to cyclic guanosine that catalyses conversion of guanosine triphophate to cyclic guanosine composphate (GGMP) and is present on the apical (air) side of respiratory epithelial cells but not on the basolateral (blood) side. CGMP activates membrane-associated type II protein kinase which in turn activates the regulatory domain of the cystic fibrosis transmembrane conductance regulator, resulting in secretion of chloride ions and water from the cells, causing fulidisation of the mucus. The products of the invention are used to make an inhalation device containing the medicament of disorders of mucus secretion in the respiratory tract, by detecting at least one GCC activator. The products of the invention have antiasthmatic disorders of mucus secretion in the respiratory tract particularly bronchial asthmatic chronic bronchitis and cystic fibrosis. The product of the invention contracts of mucus secretion in the respiratory tract particularly bronchial asthmatic contracts of the invention contracts of mucus secretion in the respiratory tract particularly bronchial sethmatic contracts of the invention contracts of the invention contracts of the invention contracts of the medicament does not enter the bloodstream), so systemic side effects are minimised. Only very small doses of the medicament are required. This sequence represents a heat stable E. coli enterotoxin contractived peptide use in an assay to determine guanylate cyclase C activation described in the disclosure of the invention

ö Gaps ö Length 19; 0; Indels Score 15; DB 6; Le Pred. No. 2.2e-09; Mismatches 78.9%; Sc._ 100.0%; Pre Conservative Similarity 15; Query Match Best Local S Matches

1 NSSNYCCELCCNPAC 15

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Search completed: March 26, 2005, 17:20:58 Job time : 85.4821 secs

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The present invention relates to a method for targeting an agent to a breast cancer cell, prostate cancer cell, a pancreatic cancer cell or melanoma cancer cell. The method involves contacting the cancer cell with stable enterotoxin (ST) motif that binds to the cancer cell. The ST motif may comprise a tail region (ADC14118) and an receptor binding region (ADC14119). The method is used for targeting an agent to breast, prostate, pancreatic or melanoma cancer cell; for rendering, treating and preventing an unresectable breast, prostate, pancreatic or melanoma tumour and for identifying tumour binding peptide. The present sequence is heat stable enterotoxin (STH) produced by human strain of Escherichia Breast cancer; prostate cancer; pancreatic cancer; melanoma; heat stable enterotoxin; ST motif; tail region; receptor binding region; Method of treating or preventing breast, prostate, pancreatic cancer or melanoma, comprises targeting peptide agent complex to breast cancer cell, prostate cancer cell, pancreatic cancer cell or melanoma cancer Gaps ; Length 19; Indels Hoffman T; 78.9%; Score 15; DB 7; Let 100.0%; Pred. No. 2.2e-09; tive 0; Mismatches 0; Forte L, Location/Qualifiers ADC14120 standard; peptide; 19 AA. Volkert W, Disclosure; Fig 1; 41pp; English. 21-FEB-2003; 2003WO-US005343. Heat stable enterotoxin, STh. 22-FEB-2002; 2002US-0359204P. 1 NSSNYCCELCCNPAC 15 1 NSSNYCCELCCNPAC 15 18-DEC-2003 (first entry) 6. .11 7. .15 10. .18. Conservative (UMOR ) UNIV MISSOURI. Gali H, WPI; 2003-731571/69. Query Match Best Local Similarity Matches 15; Conserv Escherichia coli. WO2003072125-A1 Key Disulfide-bond Disulfide-bond Disulfide-bond Sequence 19 AA; 04-SEP-2003 Sieckman G, cytostatic. ADC14120; RESULT 15 ADC14120 . 8

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1 NSSNYCCELCCNPACNGCY 19
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score:
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                                                                                OM protein
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                                                                                                                                                                                                                            Sequence:
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                                                                                                                   Run on:
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   Sequence 5, Application US/08141892A

Sequence 5, Application US/08141892A

Sequence 5, Application US/08141892A

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods

TITLE OF INVENTION: Of Using the Same

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris

STRATE: Pennsty Place - 46th Floor

CITY: Philadelphia

STRATE: Pennstylvania

CONTRY: U.S.A.

ZIP: 19103

COMPUTER: 135 inch disk, 720 Kb

COMPUTER: 18M PC compatible

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                   Sequence
Sequence
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US-08-635-930-29
US-09-139-297-29
US-08-138-237A-29
US-08-141-892A-34
US-08-673-920-34
US-08-655-930-34
US-09-138-237A-34
US-08-193-997-34
US-08-193-997-30
US-08-635-930-30
US-08-635-930-30
US-08-635-930-30
US-08-635-930-30
US-08-635-930-30
US-09-138-237A-35
US-08-138-237A-35
US-08-138-237A-35
US-08-138-237A-35
US-08-138-237A-35
US-08-138-237A-35
                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/ABENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELECOMMONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: Compositions That Specifically Bind To

TITLE OF INVENTION: Compositions That Specifically Bind To

TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using

TITLE OF INVENTION: The Same

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STRYE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION: 435
PRICR APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRICR APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INF
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ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WordPerfect 6.0/6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,930
FILING DATE: 26-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION HOMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: DELUCA, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08635930 Patent No. 6060037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-920-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-635-930-5
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                                                                                                                                                                    Sequence 5, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels
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Patent No. 5962220

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 596220ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: WILLOWS
SOFTWARE: Wordberfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-3N-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NSSNYCCELCCNPACNGCY 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibli
OPERATING SYSTEM: Windows
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COUNTRY: USA
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US-08-467-920-5
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CURRENT APPLICATION DATA:
SOFTWARE:
Wordberfect 5.1
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATORNEY/AGENT INFORMATION:
MAME: DELUCA MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-0903
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 27, Application US/08141892A
; Patent No. 5518888
   1 NSSNYCCELCCNPACNGCY 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-138-237A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compositions That Specifically
Bind To Colorectal Cancer Cell
And Methods Of Using The Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6087109ris
STREET: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 3; I
100.0%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USAN

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIPTCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIPTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REPERENCE/DOCKET NUMBER: TUU-1589
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
                                  TJU-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09193997
; Patent No. 6087109
; GENERAL INFORMATION:
    APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Eand To Color;
; TITLE OF INVENTION: Bind To Color;
; TITLE OF INVENTION: And Methods Oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NSSNYCCELCCNPACNGCY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSSNYCCELCCNPACNGCY 19
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   33,229
                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 215-568-3100
REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                   TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-635-930-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-193-997-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserv
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Sequence 5, Application US/09138237A

Patent No. 6588159

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods

TITLE OF INVENTION: Of Using the Same

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159718

STRERT: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
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APPLICANT: Waldman, Scott A.
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 551888
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 3;
Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
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Gaps
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                                                                                                                                                                                                        Length 18;
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                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Furtz Mackiewicz &
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                     DB 2; Le
1.8e-09;
                                                                                                                                                                                                  78.9%; Score 15; DB 100.0%; Pred. No. 1.8 ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT: INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJUU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/467,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08467920 Patent No. 5962220
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                                                                                                                                                                                                                                                                                                                                                            1 NSSNYCCELCCNPAC 15
                                                                                                                                                                                                                                                                                                           1 NSSNYCCELCCNPAC 15
                                           18 amino acids
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 amino acide
                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-467-920-27
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                                                                                                                                                    US-08-583-447A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-467-920-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-635-930-27
                                           LENGTH:
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; Patent No. 5879656
; GENERAL INFORMATION:
    APPLICANT: Waldman, Scott A.
    TITLE OF INVENTION: ST Receptor Binding Compounds and TITLE OF INVENTION: Methods of Using the Same NUMBER OF SEQUENCES: 56
    CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris STREET: One Liberty Place, 46th Floor CITY: Philadelphia
    STATE: Pennsylvania
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
MEDIUM TYPE: 3.5 inch disk, 720 Kb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/141,892A FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: FILING DATE: FILING DATE: FILING DATE: FILING PAPE: TOWNBER: FILING DATE: FILING PAPE: PS-568-3100
REGISTRATION NUMBER: TUU-0903
REFERENCE/DOCKET NUMBER: TUU-0903
TELEPAX: 215-568-3100
TELEPAX: 215-568-3100
TELEPAX: 215-568-3100
TELEPAX: 215-568-3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ERAPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 31,229
REGISTRATION NUMBER: 31,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NSSNYCCELCCNPAC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-141-892A-27
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US-08-583-447A-27
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Sequence 27, Application US/09138237A, Pacent No. 6268159
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS: ADDRESSE: Modcock Washburn Kurtz Mackiewicz and No. 6268159ris. STREET: One Liberty Place - 46th Floor
CITY: Philadelphia STATE: Pennsylvania
CCUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%; Score 15; DB 3; Length 18; 100.0%; Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark:
RESISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-0903
TELECHONICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
                                                                                                                                                                                                                                                                                                                                                                                                                                      TJU-1589
                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
                                                                                                                                                                                                                                                                                                       FILLING MAIS:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DefLuca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TUU-J
TELECOMMUNICATION INFORMATION:
TELEFAN: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: C15-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSSNYCCELCCNPAC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-138-237A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-193-997-27
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                                                                         Compositions That Specifically Bind To
Colorectal Cancer Cells And Methods Of Using
The Same
                                                                                                                                                  NUMBER OF SEQUENCES: 54
CORRESPONDENCE DDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
STREET: One Liberty Place, 46th Floor
STREET: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09193997
; Sequence 27, Application US/09193997
; GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically TITLE OF INVENTION: Bind To Colorectal Cancer Cells TITLE OF INVENTION: And Methods Of Using The Same NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: One Liberty Place, 46th Floor CITY: Philadelphia STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISP PC compactible
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: Wordferiect 6.0/6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,930
FILING DATE: 26-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: 08/141,892
FILING DATE: 13-58P-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
ATOMNES: 13-58P-1994
CLASSIFICATION: 435
ATOMNES: 13-58P-1994
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION NUMBER: TJU-1360
TELECOMMUNICATION NUMBER: TJU-1360
TELECOMMUNICATION NUMBER: TJU-1360
TELECOMMUNICATION NUMBER: TJU-1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                  Scott A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NSSNYCCELCCNPAC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-635-930-27
                                          APPLICANT: Waldman, STITLE OF INVENTION: CTITLE OF INVENTION: CTITLE OF INVENTION: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-193-997-27
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Gaps

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TITLE OF INVENTION: ST Receptor Binding Compounds and TITLE OF INVENTION: Methods of Using the Same NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris STREET: One Liberty Place, 46th Floor CITY: Philadelphia STATE: Pennsylvania STATE: Pennsylvania
                                                                                                                                                                                                                      ZIP: 19103

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892
FILING DATE: 26-OCT-1993
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER: US/08/141,892
FILING DATE: 26-OCT-1993
CLASSIFCATION: 345
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPOMNINICATION INFORMATION:
TELEPOMNINICATION INFORMATION:
TELEPOMNINICATION INFORMATION:
TELEPAX: 215-568-3109
TELEPAX: 215-568-3109
TELEPAX: 215-568-3109
TELEPAX: 215-568-3109
TELEPAX: 17-Amino acids
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888IS
STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                     Score 15; DB 3; Length 18; Pred. No. 1.8e-09;
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Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                    Mismatches
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STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA: DS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 1850A
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 33,229.
REGISTRATION NUMBER: 33,229.
REGISTRATION NUMBER: 33,229.
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US-08-583-447A-28
; Sequence 28, Application US/08583447A
; Setant No. 5879656
; GENERAL INPORMATION:
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Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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    SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
TYPE: amino acid
                             18 amino acids
                                                                 TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-138-237A-27
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US-08-141-892A-28
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Length 17;
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APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5562220Tis
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
73.7%; Score 14; DB 2; 100.0%; Pred. No. 1.9e-0
           100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/467,920
                                                                                                                                                                                       US-08-467-920-28
; Sequence 28, Application US/08467920
; Patent No. 5962220
                                                                            2 SSNYCCELCCNPAC 15
                                                                                                  1 SSNYCCELCCNPAC 14
Query Match
Best Local Similarity 100.
Matches 14; Conservative
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FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/141,892

FILING DATE: 26-OCT-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Debluca, Mark

REGISTRATION NUMBER: TJU-1589

REFERENCE/OMONICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHRACTERISTICS:

LENGTH: 17 amino acid

TYPE: amino acid

TYPE: amino acid

MOLECULE TYPE: peptide

US-08-467-920-28

Query Match

Guery Match

MAtches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 26, 2005, 17:27:27 Job time : 26.7857 secs

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions arrapm and trapm and trapm.

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions

ngar. bas mgar.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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March 26, 2005, 17:25:02 ; Search time 61.4107 Seconds (without alignments) 102.440 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-107-814-23
US-10-371-966-1
US-10-796-719-12
US-10-796-719-27
US-10-796-719-27
US-10-796-719-27
US-10-796-719-39
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COMPUTER: Pennsylvania
COUNTRY: USA
COMPUTER: Pennsylvania
COUNTRY: USA
COMPUTER: Pennsylvania
COMPUTER: Dennsylvania
COMPUTER: USA
COMPUTER: ENDORATION
COMPUTER: USA
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US-10-621-684-5
i Sequence 5, Application US/10621684
j Publication No. US20040029182A1
j GENERAL INFORMATION:
i GENERAL INFORMATION:
j TITLE OF INVENTION: ST Receptor Binding Compounds and
i TITLE OF INVENTION: ST Receptor Binding Compounds and
US-10-621-684-33

US-10-621-684-29

US-10-621-684-35

US-10-621-684-31

US-10-621-684-31

US-10-621-684-13

US-10-621-684-13

US-10-621-684-14

US-10-621-684-16

US-10-621-684-16

US-10-621-684-15

US-10-621-684-15

US-10-621-684-15

US-10-621-684-15

US-10-621-684-14

US-10-621-684-14

US-10-621-684-14

US-10-621-684-14

US-10-621-684-14

US-10-621-684-19

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REGISTRATION NUMBER: 33,229
REGISTROF/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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Sequence

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APPLICANT: SIECECAAN,
APPLICANT: SIECECAAN,
APPLICANT: FOREE, LEONARD
APPLICANT: FOREE, LEONARD
APPLICANT: HOFFMAN, TIMOTHY
APPLICANT: GALI, HARIPRASAD
TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
FILE REPERRANCE: UVMO:013US
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/359,204
PRIOR APPLICATION NUMBER: 60/359,204
PRIOR APPLICATION NUMBER: 60/359,204
PRIOR APPLICATION NUMBER: 2003-02-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver: 2.1
                                     Sequence 23, Application US/10107814

Fublication No. US20030073628A1

GENERAL INFORMATION:

APPLICANT: SHALUBHAI, KUNWAR

APPLICANT: MIKIFOROVICH, GREGORY

APPLICANT: JACOB, GARY S.

TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS

TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS

FILE REFERENCE: 81361/284943/MAS

CURRENT APPLICATION NUMBER: US/10/107,814

CURRENT APPLICATION NUMBER: US/10/107,814

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATCHIL VOY: 2.1

FEASO ID NO 23

FEASO ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-371-966-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 15; DB 14; I 100.0%; Pred. No. 2.4e-09; ive 0; Mismatches 0;
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100.0%; Pred. No. 2.4e-09;
tive 0; Mismatches 0;
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; Publication No. US20030232013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NSSNYCCELCCNPAC 15
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Escherichia coli
PEATURE:
NAME/KEY: DISULFID
LOCATION: (6)..(10)
NAME/KEY: DISULFID
LOCATION: (7)..(15)
NAME/KEY: DISULFID
LOCATION: (11)..(18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.9 Best Local Similarity 100. Matches 15; Conservative
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nes 15; Conserv
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Matches
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ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
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US-10-621-684-27
Sequence 27, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION:
                                                                                                                                                                                                                          Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.9%; Score 15; DB 15; Length 18; 100.0%; Pred. No. 2.3e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION UNDER: US/08/583,447A
APPLICATION UNDER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 27: US-10-621-684-27
                                                               TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids TYPE: amino acid
                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                   1 NSSNYCCELCCNPACNGCY 19
                                                                                                                                                                                                                                                                                                                                                                1 NSSNYCCELCCNPACNGCY 19
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS
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Matches 15, Conserv
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Sequence 27, Application US/10796719

Sequence 27, Application US/10796719

Publication No. US20050020811A1

GENERAL INFORMATION:

APPLICANT: Currie, Mark G.

APPLICANT: Mahajan-Miklos, Shalina

TITLE OF INVENTION: TREATHENT OF GASTROINTESTINAL DISORDERS

TITLE OF INVENTION: TREATHENT OF GASTROINTESTINAL DISORDERS

TILE REFERENCE: 14184-043001

CURRENT APPLICATION NUMBER: US/10/796,719

CURRENT APPLICATION NUMBER: US/04-03-09

FRIOR FILING DATE: 2004-03-09

PRIOR FILING DATE: 2004-01-28

PRIOR FILING DATE: 2003-01-28

PRIOR FILING DATE: 2003-01-28

PRIOR FILING DATE: 2003-01-28

PRIOR FILING DATE: 2003-01-12

PRIOR FILING DATE: 2003-01-12

PRIOR PELIORION NUMBER: US 60/471,288

PRIOR FILING DATE: 2003-01-12

NUMBER OF SEQ ID NOS: 149

SEQ ID NO 27

LENGTH: 19

LENGTH: 19
                                                                                                                                 APPLICANT: MAILE, MAIKLOS, SHAILIAA
TITLE OP INVENTION: TRETHOUS AND COMPOSITIONS FOR THE
TITLE OP INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US/10/796,719
FRIOR APPLICATION NUMBER: US/10/66,735
PRIOR PILING DATE: 2004-01-28
FRIOR PILING DATE: 2004-01-28
FRIOR PILING DATE: 2003-01-28
FRIOR PILING DATE: 2003-01-28
FRIOR PILING DATE: 2003-01-28
FRIOR PILING DATE: 2003-01-18
FRIOR APPLICATION NUMBER: US 60/411,288
FRIOR APPLICATION NUMBER: US 60/519,460
FRIOR APPLICATION NUMBER: US 60/519,460
FRIOR PILING DATE: 2003-11-12
NUMBER OF SEQ ID NOS: 149
SEQ ID NO 26
LENGHARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Syntheticaly generated peptide
US-10-796-719-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.9%; Score 15; DB 17; Best Local Similarity 100.0%; Pred. No. 2.4e-09; Matches 15; Conservative 0; Mismatches 0;
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US-10-796-719-27
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  US-10-796-719-26
; Sequence 26, Application US/10796719
; Publication No. US205020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                   APPLICANT: SIECKGAN, GARY
APPLICANT: SIECKGAN, GARY
APPLICANT: FORTE, LEDGARD
APPLICANT: FORTE, LEDGARD
APPLICANT: HOFFMAN, TIMOTHY
APPLICANT: HOFFMAN, TIMOTHY
APPLICANT: HOFFMAN, TIMOTHY
APPLICANT: GALI, HARIERAABA
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
FILE REFERENCE: UNMO:013US
CURRENT APPLICATION NUMBER: US/10/371,966
FRIOR APPLICATION NUMBER: 60/359,204
PRIOR FILING DATE: 2003-02-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATEURIN VEY: 2.1
SEQ ID NO 2.
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Publication No. US20050020811A1

GENERAL INFORMATION:

APPLICANT: Currie, Mark G.

APPLICANT: Currie, Mark G.

TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS

TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS

FILE REFERENCE: 14184-043001

CURRENT APPLICATION NUMBER: US/10/796,719

FURBANT RILING DATE: 2004-03-09

PRIOR FILING DATE: 2004-01-28

PRIOR FILING DATE: 2003-01-28

PRIOR PLICATION NUMBER: US 60/443,098

PRIOR FILING DATE: 2003-01-28

PRIOR PLICATION NUMBER: US 60/471,288

PRIOR FILING DATE: 2003-01-28

PRIOR FILING DATE: 2003-01-12

SOFTWARE FREE SEQUENCE: 149

SOFTWARE FREE SECUENCE: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Score 15; DB 15; Length 19; 100.0%; Pred. No. 2.4e-09; tive 0; Mismatches 0; Indels
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Sequence 2, Application US/10371966
Publication No. US20030232013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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US-10-796-719-1
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SEQ ID NO 1

US-10-371-966-2 Query Match

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| Sequence 21, Application US/10796719
| Publication No. US20050020811A1
| GENERAL INFORMATION:
| APPLICANT: Currie, Mark G.
| APPLICANT: Mahajan-Miklos, Shalina APPLICANT: Mahajan-Miklos, Shalina TITLE OF INVENTION: TREATHENDS AND COMPOSITIONS FOR THE TITLE OF INVENTION: TREATHENDY OF GASTROINTESTINAL DISORDERS FILE REFERENCE: 14184-043001
| CURRENT FILING DATE: 2004-03-09
| CURRENT PILING DATE: 2004-01-28
| PRIOR FILING DATE: 2004-01-28
| PRIOR FILING DATE: 2003-01-28
| PRIOR FILING DATE: 2003-01-28
| PRIOR PLICATION NUMBER: US 60/443,098
| PRIOR PLICATION NUMBER: US 60/471,288
| PRIOR PLING DATE: 2003-01-28
| PRIOR FILING DATE: 2003-01-128
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gurrie, Mark G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Mahajan-Miklos, Shalina
TITLE OF INVENTION: METREATMENT OF GASTROINTESTINAL DISORDERS
TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US 10/766,735
PRIOR APPLICATION NUMBER: US 60/443,098
PRIOR FILING DATE: 2004-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: US 60/411,288
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2003-01-12
PRIOR FILING DATE: 2003-01-12
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
   0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Syntheticaly generated peptide US-10-796-719-40
   Mismatches
                                                                                                                                                                                                                                                                                         Sequence 40, Application US/10796719
Publication No. US20050020811A1
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                                                                   1 NSSNYCCELCCNPAC 15
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15; Conservative
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, ORGANISM: Escherichia coli
US-10-796-719-21
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   Matches
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TITLE OF INVENTION: Quanylate-cyclase C ligand, administered via the airways, for the
TITLE OF INVENTION: treatment of respiratory airway problems
FILE REFERENCE: 03100192aa
CURRENT PELING DATE: 2003-12-04
PRIOR PAPLICATION NUMBER: US/10/479,606
CURRENT FILING DATE: 2003-10-04
PRIOR PELICATION NUMBER: DE10127119.0
PRIOR PILING DATE: 2003-06-05
PRIOR PELICATION NUMBER: PCT/DE02/02040
PRIOR PILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NO 7
LENGTH: 19
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                                        Gaps
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US-10-796-719-39
is Sequence 39, Application US/10796719
is Sequence 39, Application US/10796719
is Publication No. US20050020811A1
is GENERAL INFORMATION:
is APPLICANT: Outrie, Mark G.
itTLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
itTLE OF INVENTION: METHODS AND COMPOSITION FOR THE
itTLE OF INVENTION UNMERR: US/10/796,719
iCURRENT APPLICATION NUMBER: US 60/413,098
iPRIOR PILING DATE: 2004-01-28
iPRIOR APPLICATION NUMBER: US 60/471,288
iPRIOR FILING DATE: 2003-10-12
iPRIOR FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.9%; Score 15; DB 17; Length 21; 100.0%; Pred. No. 2.6e-09;
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                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.4e-09; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.9%; Score 15; DB 17; Best Local Similarity 100.0%; Pred. No. 2.4e-09; Matches 15; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Syntheticaly generated peptide
US-10-796-719-39
                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10479606
Publication No. US20050032684A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                          1 NSSNYCCELCCNPAC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cetin, Yalcin
APPLICANT: Savas, Yuksel
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Best Local Similarity
                                                                                                                                                                                                                                                                 RESULT 9
US-10-479-606-7
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LENGTH: 21
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
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Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; L
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.7%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 2.7
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                        ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
                                                                                                     STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
NUMBER OF SEQUENCES: 56
                                                                                CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-621-684-33
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                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182Alris
STREET: One Liberty Place, 46th Floor
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                                                            Gaps
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5.10-621-684-28

Sequence 28, Application US/10621684

Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and

Methods of Using the Same
                 Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott A.
ST Receptor Binding Compounds and
Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
                                                            0; Indels
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                   DB 17; L
6.6e-09;
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100.0%; Pred. No. 2.6e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-JUL-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-621-684-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
  78.9%; Scc..
100.0%; Pre
0;
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Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Recepte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                          54 NSSNYCCELCCNPAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SSNYCCELCCNPAC 15
            Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Matches 14; Conserva
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APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
FILING DATE: 05-JAN-1996
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INPORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DCCKET NUMBER: TJU-1702
FILEPROMENUNICATION INFORMATION:
FILEFRAX: 215-568-3100

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1 SNYCCELCCNPAC 13
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Search completed: March 26, 2005, 17:44:31 Job time : 61.4107 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein March 26, 2005, 17:10:31 ; Search time 19.6786 Seconds (without alignments) 92.899 Million cell updates/sec Run on:

US-10-775-481A-5 19

NSSNYCCELCCNPACNGCY 19 Perfect score: Sequence:

Scoring table:

ত্যিউত্তি Gapop 60.0 , Gapext 60.0

283416 segs, 96216763 residues Searched:

0 Word size : Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8 Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	15	78.9	72	-	QHEC4	heat-stable ente
7	15	78.9	72	Н	QHECIB	
m	11	57.9	. 18	~	A60103	
4	11	57.9	72	٦	QHEC1 .	heat-stable ente
S	10	52.6	53	~	S68705	
9	7	36.8	18	Н	QHEC2	heat-stable ente
7	7	36.8	248	~	T19913	hypothetical pro
89	9	31.6	13	N	A28953	alpha-conotoxin
σ	9	31.6	15	ч	NTKNAG	alpha-conotoxin
10	9	31.6	17	~	A54534	heat-stable ente
11	9	31.6	19	~	A44379	alpha-conotoxin
12	9	31.6	65	~	S34671	heat-stable ente
13	9	31.6	99	7	831652	enterotoxin - Ye
14	9	31.6	71	~	S25659	heat-stable ente
15	9	31.6	78	-	QHVC1	
16	9	31.6	124	ч	NRPG .	pancreatic ribon
17	9	31.6	128	-	NRGPB	pancreatic ribon
18	9	31.6	136	~	T16269	hypothetical pro
19	9	31.6	408	~	T37929	probable major f
20	ø	31.6	796	~	T20091	hypothetical pro
21	'n	26.3	75	7	H84631	hypothetical pro
22	Ŋ	26.3	90	~	D85845	
23	ß	26.3	110	~	174319	gene EHS-2 prote
24	S	26.3	116	~	877004	
25	2	26.3	118	~	D97733	hypothetical pro
56	S	26.3	122	-	NRKGR	-~
27	S	26.3	124		NRBOB	pancreatic ribon
28	Ŋ	26.3	124	-	NRANE	
53	'n	26.3	124	Н	NRDEF	pancreatic ribon

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NRDEN NRDEO NRDER NPEKN	NRGF NRGN NRGT NR PRH	NRSH NRWB S07141 S08547	S08546 S08549 C96762 A86872
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26.3 26.3 26.3	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	26.3 26.3 26.3	26.3 26.3 26.3
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30 32 32 33	1 M M M M	388 398 110	4 4 4 4 ሪ ພ 4 ሲ

## ALIGNMENTS

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C;Accession: JT0373; A35578
R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
B;Stieglitz, H.; Cervantes, L.; Bolivar, F.;
A;Title: Cloning, sequencing, and expression in ficoll generated minicells of an Escheria, A;Reference number: JT0373; MUID:89202548; PMID:3071819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: __UNIPROT:P07965; GB:J03311; NID:g147875; PIDN:AAA24652.1; PID:g147876
R;Ahou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stabla;Reference number: A35978; MUID:90273381; PMID:2190361
                            C.Species: Escherichia coli
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: heat-stable enterotoxin ST
C;Kbywords: enterotoxin; heat-stable protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-53/Domain: propertiod #status predicted <PRO>
F;54-72/Product: heat-stable enterotoxin #status predicted <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status predicted
heat-stable enterotoxin STA4 precursor - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-72 <STI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-72 <ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A35978
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A;Gene: estA4

ö Length 72; 0; Indels DB 1; Le Mismatches Score 15; Pred. No. 78.55, 100.0%; Pre-Local Similarity 100. Query Match Matches

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Gaps

15 54 NSSNYCCELCCNPAC 68 1 NSSNYCCELCCNPAC 용 ઠ

RESULT 2

heat-stable enterotoxin ST-Ib precursor - Escherichia coli
NiAlternate names: heat-stable enterotoxin ST-A2
NiAlternate names: heat-stable enterotoxin ST-A2
Cispecies Bscherichia coli
Cispecies Bscherichia coli
Cispecies 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
CiAccession: JS0292; A33068; A33067; A30567
Rimoseley, S.L.; Hardy, U.W.; Huq, M.I.; Echeverria, P.; Falkow, S.
Infect: Immun. 39, 1167-1174, 1983
A;Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterot
A;Reference number: JS0292; MUID:83184648; PMID:6341230

A; Accession: JS0292 A; Molecule type: DNA

```
C;Species: Escherichia coli
C;Date: 31-Aug-1980 #sequence revision 31-Aug-1980 #text_change 09-Jul-2004
C;Accession: A01822; A30985; A36732; JT0374; I51932
R;So, M:; McCarthy, B.J.
Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
Prof. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
A;Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stale (S7 A;Reference number: A01822; MUID:81054703; PMID:6254008
                                                                                                                                                                                                                                                                                                                A.Molecule type: DNA
A;Residues: 1-72 <LAZ>
A;Crostones: 1072 <LAZ>
A;Crostones: UNIPROT:P01559; GB:V00612; GB:J01831; NID:g43704; PIDN:CAA23883.1; PJ
A;Crostones. C.; Seddah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.
Can. J. Biochem. Cell Biol. 61, 287-292, 1983
A;Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of FA;Reference number: A30985; MUID:83284515; PMID:6349752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-72 - CDAL>
A; Cross-references: GB: MS8746; NID:g145860; PIDN:AAA62776.1; PID:g145861
A; Experimental source: strain 18D
B; Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Flasmid 20, 42-53, 1988
A; Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheric A; Reference number: JT0373; MUD:89202548; PMID:3071819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for Escherichia coli heat-stable enterotoxin 1|
PMID:2990268
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;Residues: 1-69,'P',71-72 «RES»
;Cross-references: GB:M25607; NID:g147877; PIDN:AAA24653.1; PID:g147878
;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568705
heat-stable enterotoxin Y-STC - Yersinia enterocolitica
heat-stable enterotoxin Y-STC - Yersinia enterocolitica
C;Species: Yersinia enterotoxin X:7 Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FBBS Lett. 362, 319-322, 1995
A;Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A;Reference number: S68705; MUID:95246844; PMID:7729521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C;Keywords: enterotoxin; heat-stable protein
C;F;1-19/Domain: signal sequence #status predicted <SIG>
F;2-74/Domain: propeptide #status predicted <PRO>
F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status predicted
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A;Molecule type: protein
A;Residues: 2-72 <1A22-
A;Essidues: Strain F11
B;Dallas, W.S.
J; Bacteriol. 172, 5490-5493, 1990
A;Reference number: A36732; MUID:90368614; PMID:2203756
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Pred. No. 7.2e-06;
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;Residues: 1-72 <STI>
;Sekizaki, T.; Akashi, H.; Terakado, N.
m. J. Vet. Res. 46, 909-912, 1985
;Title: Nucleotide sequences of the genes
;Reference number: 151932; MUID:85249571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.9%; Scc.
100.0%; Pre/
0; N
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Best Local S:
Matches 11
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A;Residues: 1-72 <MOS>
A;Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:g146407; PIDN:AAA2399; GB:Waxahath, P: Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagamnatha, Gane 81, 219-226, 1989
Gane 81, 219-226, 1989
A;Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escheriancession: A33068
A;Reference number: A33068; MUD:90034194; PMID:2680769
A;Residues: 1-18,'A', 20-72 < DWA>
A;Reference authors: A33067; WUID:83105138; PMID:6759126
A;Aritle: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenian A;Reference number: A33067; WUID:83105138; PMID:6759126
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A64103
A64103
A64104
A60103
A64104
A67109
A67109
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Accession: A60103
A;Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical A;Reference number: A60103; MUD:89108617; PMID:2912902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 54-72 <AIM>
A;Residues: 54-72 <AIM>
Kiguzman-Verduzco, L.M.; Kupersztoch, Y.M.
Infect. Immun. 57, 645-648, 1989
A;Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
A;Reference number: A30567; MUID:89108616; PMID:2643580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
KICOSS-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C;Genetics:
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$1.53/Domain: slignal sequence and propeptide #status predicted <SIG>
F;54-72/Product: heat-stable enterotoxin $T-1b #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status experimental
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N;Alternate names: heat-stable enterotoxin estAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: heat-stable enterotoxin ST
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C;Superfamily: heat-stable enterotoxin ST
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A,Molecule type: protein
A,Residues: 1-18 <GUA>
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Best Local Similarity
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Matches

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Best Loca Matches

RESULT 4

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A;Molecule type: protein
A;Residues: 1-13 <ZAF>
A;Cross-teferences: UNIPROT:p15471
A;Note: this sequence was confirmed by chemical synthesis
C;Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin
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A; Kestauces: 1-15 Cura.,
A; Cross-references: UNIPROT: P01519
R; Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
Biol. Chem. 258, 1224-12231, 1983
A; Title: Conotoxin MI. Disulfide bonding and conformational states.
A; Reference number: A92396; MUID: 84032400; PMID: 6630187
A; Rothers: annotation; disulfide bonds
R; Guddat, L.W.; Shan, L.; Martin, J.L.; Edmudson, A.B.; Gray, W.R.
Submitted to the Brookhaven Protein Data Bank, May 1996
A; Reference number: A6523; PBBINOT
A; Reference number: A5523; PBBINOT
A; Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13
R; Guddat, L.W.; Martin, J.A.; Shan, L.; Edmudson, A.B.; Gray, W.R.
B; Guddat, L.W.; Martin, J.A.; Shan, L.; Edmudson, A.B.; Gray, W.R.
A; Contents: annotation; X-ray crystallography, 1.2 angstroms
A; Reference number: A58592; MUID: 96378624; PMID: 8784187
A; Reference number: A36592; MUID: 96378624; PMID: 8784187
A; Flitle: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spe
A; Contents: annotation; conformation by (i)H-NMR
C; Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
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C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl en
F;1-15/Product: conotoxin GIA #status experimental <GIA>
F;1-13/Product: conotoxin GI #status experimental <GIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot
F;2-7,3-13/Disulfide bonds: #status experimental
F;13/Modified site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                         B.M.; Cruz, L.J.
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                                                                                                                                                                                                                                                                                                          C;Accession: A28953
R;Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz
Biochemistry 27, 7102-7105, 1988
A;Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
A;Reference number: A28953; MUID:89062448; PMID:3196703
                                                                                                                                                                                                    alpha-conotoxin SI - cone shell (Conus striatus)
C;Species: Conus striatus (striated cone)
C;Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Conus geographus (geography cone)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
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A;Title: Peptidde toxins from Conus geographus venom.
A;Reference number: A92320; MUID:81191854; PMID:7014556
A;Accession: A01782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cone shell (Conus geographus)
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100.0%; Pred. No. 1.1;
rative 0; Mismatches
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               181 SSNYCCE 187
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Best Local Similarity
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Cispectes: Caenorhabditis elegans
Cispectes: Caenorhabditis elegans
Cispectes: Caenorhabditis elegans
Cispectes: Caenorhabditis elegans
Cispectes: Caenorhabditis elegans
Cispectes: T19913
R.Mortimore, B.
submitted to the EMBL Data Library, November 1996
A.Reference number: 219195
A.Reference number: 219195
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: DNA
A.Residues: 1-248 «MLL»
A.Cross-references: UNIPROT:Q9XUG6; EMBL:282262; PIDN:CAB05152.1; GSPDB:GN00022; CESP:C4
A.Gene: CESP:C43F9.5
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                                                                                                                                                                                                                                                                       52.6%; Score 10; DB 2; Length 53; ilarity 100.0%; Pred. No. 8e-05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 248;
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A;Molecule type: protein
A;Residues: 1-53 <YOS>
A;Residues: 10x3 <YOS>
C;Superimental source: strain 86-11
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;41-46,42-50,45-53/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C43F9.5 - Caenorhabditis elegans
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100.0%; Pred. No. 0.098;
ive 0; Mismatches 0
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100.0%; Pred. No. 0.68;
iive 0; Mismatches
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Best Local Similarity 100.v
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Best Local Similarity luv...
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nes 10; Conserv
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Best Local S:
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C;Accession: 534671
R;Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.
Bubmitted to the EMBL Data Library, July 1993
A;Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymerae A;Reference number: S34671
A;Accession: 534671
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R;Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R.
Infect. Immun. 58, 2983-2988, 1990
A;Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-fa;Reference number: A41474; MUID:90354067; PMID:2201642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-66 <-IBR>
A, Cross-references: UNIPROT: P21518; EMBL: X69218; NID: g48617; PIDN: CAA49152.1; PID: g48618
C; Superfamily: heat-stable enterotoxin ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Yerainia enterocollitica
C;Species: Yerainia enterocollitica
C;Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 825659; Ad144; A21314; 865849
R;Ibrahim, A; Liesack, W.; Pike, S.; Stackebrandt, E.
FEMS Microbiol. Lett. 97, 63-66, 1992
A;Title: The polymerase chain reaction: an epidemiological tool to differentiate between
A;Reference number: 825659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat-stable enterotoxin yst precursor - Yersinia enterocolitica
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A;Residues: 1-47,'S',49-71 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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100.0%; Pred. No. 3.6;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 31.6%; Score 6; DB 2;
100.0%; Pred. No. 3.5;
tive 0; Mismatches
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C; Superfamily: heat-stable enterotoxin ST
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                C; Species: Vibrio cholerae
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-65 <ROS>
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F;2-7,3-13/{\rm Disulfide} bonds: #link GIA #status predicted F;2-7,3-13/{\rm Disulfide} bonds: #link GIC #status experimental F;13/{\rm Modified} site: amidated carboxyl end (Cys) (amide in mature form from following gly F;13/{\rm Modified} site: blocked carboxyl end (Lys) (probably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                       A54534
C;Species Vibrio mimicus (fragment)
C;Species Vibrio mimicus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C;Accession: A54534
R;Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
R;Arita, Microbiol. Lett. 79, 105-110, 1991
A;Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicutal Reference number: A54534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: CAS:143294-31-9; PIDN:AAB23762.1; PID:g257934
A; Experimental source: venom
A; Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by che
C; Comment: This peptide is an acetylcholine receptor blocker.
C; Superfamily: alpha-conocoxin
C; Keywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom
F; 2-18, 3-8, 4-14/Disulfide bonds: #status predicted
F; 19/Modified site: amidated carboxyl end (Ser) #status absent
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alpha-conotoxin SII - cone shell (Conus striatus)
c;Species: Conus striatus (striated cone)
c;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A44379
R;Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, N Biochemistry 31, 9919-9926, 1992
A;Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A;Reference number: A44379; MUD:93003172; PMID:1390774
A;Molecule type: protein
A;Residues: 1-19 cRAM>
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100.0%; Pred. No. 1.2;.
tive 0; Mismatches
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100.0%; Pred. No. 1.3;
tive 0; Mismatches
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31.6%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 6; Conservative 0; Mismatches
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A,Status: preliminary
Molecule type: protein
A,Residues: 1-17 <ARL>
C,Superfamily: heat-stable enterotoxin ST
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Best Local Similarity 100.(
Matches 6, Conservative
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A;Cross-references: ĠB:U09235; NID:g487394; PIDN:AAA18472.1; PID:g487395 R;Takao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.

RESULT 12 834671 heat-stable enterotoxin - Vibrio cholerae (fragment)

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C; Superfamily: heat-stable enterotoxin ST
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Bur. J. Biochem. 152, 199-206, 1985

A;Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced A;Recensence number: A23114; MUID:86004705; PMID:4043080

A;Accession: A23114

A;Molecule type: protein

A;Residues: 54-71 < TRK>

R;Mikulskis, A.V.; Delor; I.; Ha Thi, V.; Cornelis, G.R.

Mol. Microbiol. 14, 905-915, 1994

A;Title: Regulation of the Yersinia enterocolitica enterotoxin Yst gene. Influence of gr A;Reference number: 865849; MUID:95231297; PMID:7715452

A;Accession: 865849

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Cross-references: EMBL:U09235

C;Genetics:
A;Gene: yet

C;Superfamily: heat-stable enterotoxin ST

F;1-19/Domain: signal sequence: #status predicted <8IG>
F;20-41/Domain: propeptide #status predicted <PRO>
F;20-41/Domain: propeptide #status predicted <PRO>
F;20-41/Domain: propeptide
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A;Residues: 1-78 <OGA>
A;Residues: 1-78 <OGA>
A;Residues: 1-78 <OGA>
A;Residues: 1-78 <OGA>
A;Crose-references: UNIPROT: P04429; GB:M85198; GB:M36061; NID:g155237; PIDN: AAA64889.1;
B;Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda, FEBS Lett. 193, 250-254, 1985
A;Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-A;Reference number: A01824; MUID:86056320; PMID:4065341
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Heat-stable enterotoxin ST precursor - Vibrio cholerae

C;Species: Vibrio cholerae

C;Species: Vibrio cholerae

C;Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A41469; A01824; S34464; S34466; S34465; S34463

C;Accession: A41469; A01824; S34464; S34466; S34463

C;Accession: A325-3329, 1990

A;Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio A;Reference number: A41469; MUID:90382953; PMID:2205577
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A; Readdues: 62-78 c.PR.
A; Experimental source: non-0:1 serovar
R; Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.;
PEBS Lett. 326, 81-86, 1993
A; Telle: Purification and sequence determination of heat-stable enterotoxin elaborated
A; Reference number: $34463; MUID:93314823; PMID:8325391
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100.0%; Pred. No. 3.8;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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A,Molecule type: protein
A,Residues: 61-78 <Y03>
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A;Status: preliminary
A;Molecule type: protein
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 62-78 < Y04>
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C;Keywords: enterotoxin; heat-stable protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-61/Domain: propeptide #status predicted <PRO>
F;62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
F;64-69,65-73,68-76/Disulfide bonds: #status predicted
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                                                                                                                                Length 78;
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100.0%; Pred. No. 4;
tive 0; Mismatches
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Matches 6; Conserv
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68 CCNPAC 73
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